

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 32.5171 Seconds  
(without alignments)  
165.965 Million cell updates/sec

Title: US-09-843-221A-161  
Perfect score: 34  
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28  
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*
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- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*
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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	34	100.0	34	4	AAP30022		Human parathyroid-
2	34	100.0	34	6	AAP50377		[Met (O) 8,18]hPTH- (
3	34	100.0	34	7	AAP60031		Sequence of the fi
4	34	100.0	34	11	AAR07919		Human parathyroid
5	34	100.0	34	13	AAR22283		Parathyroid hormon
6	34	100.0	34	14	AAR41549		[D-Ser3]hPTH (1-34
7	34	100.0	34	14	AAR41570		[Gln25]hPTH (1-34)
8	34	100.0	34	15	AAR58291		[Lys(For)26, Lys(F
9	34	100.0	34	15	AAR58228		[D-Asp30]-hPTH(1-3
10	34	100.0	34	15	AAR58016		N-alpha-Isopropyl-
11	34	100.0	34	15	AAR58017		[Lys(N-epsilon-Iso
12	34	100.0	34	15	AAR55724		Parathormone N-ter
13	34	100.0	34	16	AAR74521		Human parathyroid
14	34	100.0	34	17	AAW99449		Human parathyroid
15	34	100.0	34	17	AAR99978		Human parathyroid
16	34	100.0	34	17	AAR98951		Target peptide (PT
17	34	100.0	34	17	AAR98966		PTH(1-34). Not sp
18	34	100.0	34	17	AAR88835		Human parathyroid
19	34	100.0	34	18	AAW24273		Wild type parathyr
20	34	100.0	34	18	AAW19994		Cyclised human par
21	34	100.0	34	18	AAW20000		Cyclised human par
22	34	100.0	34	18	AAW20006		Cyclised human par
23	34	100.0	34	19	AAW67291		Parathyroid hormon
24	34	100.0	34	19	AAW61658		Parathyroid hormon
25	34	100.0	34	19	AAW65975		Human parathyroid
26	34	100.0	34	20	AAY50593		Resin bound cyclic
27	34	100.0	34	20	AAY17752		Human parathyroid
28	34	100.0	34	20	AAY14151		Human parathyroid
29	34	100.0	34	20	AAY02579		N-terminal 34 resi
30	34	100.0	34	20	AAW81871		Human PTH N-termin
31	34	100.0	34	21	ABJ10712		Human parathyroid
32	34	100.0	34	21	AAB07454		Amino acids 1-34 o
33	34	100.0	34	21	AAY98017		Human amino-termin
34	34	100.0	34	21	AAY82631		Human parathyroid
35	34	100.0	34	21	AAY68763		Amino acids 1-34 o
36	34	100.0	34	22	AAB84778		Native rat parathy
37	34	100.0	34	22	AAB96898		Human parathyroid
38	34	100.0	34	22	AAB81079		Human parathyroid
39	34	100.0	34	22	AAB91098		Parathyroid hormon
40	34	100.0	34	23	ABJ05328		Human PTH(1-34) pe
41	34	100.0	34	23	AAE23727		Human parathyroid
42	34	100.0	34	23	ABB06329		Human parathyroid
43	34	100.0	34	23	ABB08595		C-terminal truncat
44	34	100.0	34	23	AAE18395		Human PTH peptide
45	34	100.0	34	23	ABB07147		Parathyroid hormon
46	34	100.0	34	23	AAU73028		Parathyroid hormon
47	34	100.0	34	24	ABP71500		Human parathyroid
48	34	100.0	34	24	ABG74235		Human parathyroid
49	34	100.0	35	22	AAB91112		Parathyroid hormon
50	34	100.0	35	23	AAU73172		Parathyroid hormon

51	34	100.0	36	14	AAR39450	Ser-Val- (hPTH 3-35
52	34	100.0	36	15	AAR58286	[D-Leu24] -hPTH (1-3
53	34	100.0	36	15	AAR58292	[D-Lys27] -hPTH (1-3
54	34	100.0	36	15	AAR58293	[D-Leu28] -hPTH (1-3
55	34	100.0	36	15	AAR58294	[D-Phe34] -hPTH (1-3
56	34	100.0	36	15	AAR58295	[D-Val35] -hPTH (1-3
57	34	100.0	36	15	AAR58296	[Ala35] -hPTH (1-36)
58	34	100.0	36	15	AAR58297	[Pro35] -hPTH (1-36)
59	34	100.0	36	15	AAR58298	[NMeVal35] -hPTH (1-
60	34	100.0	36	15	AAR58299	[Thr35,Ala36] -hPTH
61	34	100.0	36	15	AAR58300	[D-Ala36] -hPTH (1-3
62	34	100.0	36	15	AAR58301	[NMeAla36] -hPTH (1-
63	34	100.0	36	15	AAR58260	[D-Val2] -hPTH (1-36
64	34	100.0	36	15	AAR58263	[D-Ile5] -hPTH (1-36
65	34	100.0	36	15	AAR58264	[D-Gln6] -hPTH (1-36
66	34	100.0	36	15	AAR58265	[D-Leu7] -hPTH (1-36
67	34	100.0	36	15	AAR58270	[D-Leu11] -hPTH (1-3
68	34	100.0	36	15	AAR58272	[D-Lys13] -hPTH (1-3
69	34	100.0	36	15	AAR58273	[D-Leu15] -hPTH (1-3
70	34	100.0	36	15	AAR58276	[Met (O2)18] -hPTH (1
71	34	100.0	36	15	AAR58278	[D-Met18] -hPTH (1-3
72	34	100.0	36	15	AAR58280	[D-Arg20] -hPTH (1-3
73	34	100.0	36	15	AAR58281	[D-Val21] -hPTH (1-3
74	34	100.0	36	15	AAR58284	[D-Trp23] -hPTH (1-3
75	34	100.0	36	15	AAR58227	[D-Gln29] -hPTH (1-3
76	34	100.0	36	15	AAR58230	[D-Val31] -hPTH (1-3
77	34	100.0	36	15	AAR58233	[D-His32] -hPTH (1-3
78	34	100.0	36	15	AAR58235	[D-Asn33] -hPTH (1-3
79	34	100.0	36	15	AAR58237	[NMePhe34] -hPTH (1-
80	34	100.0	36	15	AAR58238	[D-Asp30] -hPTH (1-3
81	34	100.0	36	15	AAR58242	[Lys (Isopropyl)13]
82	34	100.0	36	15	AAR58246	Acetyl-hPTH (1-36) -
83	34	100.0	36	15	AAR58249	[D-Ser1] -hPTH (1-36
84	34	100.0	36	15	AAR58196	[D-Phe34, D-Ala36]
85	34	100.0	36	15	AAR58198	[D-Ser3] -hPTH (1-36
86	34	100.0	36	15	AAR58199	[D-Glu4] -hPTH (1-36
87	34	100.0	36	15	AAR58200	[D-His9] -hPTH (1-36
88	34	100.0	36	15	AAR58202	[D-Asn10] -hPTH (1-3
89	34	100.0	36	15	AAR58210	[D-His14] -hPTH (1-3
90	34	100.0	36	15	AAR58211	[D-Asn16] -hPTH (1-3
91	34	100.0	36	15	AAR58213	[D-Ser17] -hPTH (1-3
92	34	100.0	36	15	AAR58215	[D-Glu19] -hPTH (1-3
93	34	100.0	36	15	AAR58220	[D-Lys26] -hPTH (1-3
94	34	100.0	36	15	AAR58171	[N-Me-Ser1] -hPTH (1
95	34	100.0	37	12	AAR11882	Parathyroid hormon
96	34	100.0	37	13	AAR24778	hPTH (1-37) -amide/e
97	34	100.0	37	15	AAR58244	[Ala0] -hPTH (1-36) -
98	34	100.0	37	15	AAR58245	[Pro0] -hPTH (1-36) -
99	34	100.0	37	22	AAB86226	Human parathyroid
100	34	100.0	37	22	AAB86229	Human parathyroid
101	34	100.0	37	23	ABB82203	Human parathyroid
102	34	100.0	38	15	AAR58282	[Trp (SO2Pmc) 23] -hP
103	34	100.0	38	15	AAR58283	[Trp (Pmc) 23] -hPTH (
104	34	100.0	38	15	AAR58018	Isopropyl- [Lys (Iso
105	34	100.0	38	15	AAR54234	PTH N-terminal. S
106	34	100.0	38	20	AAV02580	N-terminal 38 resi
107	34	100.0	38	22	AAB91101	Parathyroid hormon

108	34	100.0	38	23	AAE23729	Human parathyroid
109	34	100.0	38	23	AAE18400	Human PTH peptide
110	34	100.0	38	23	AAU73026	Parathyroid hormon
111	33	97.1	33	21	AAV98018	Human amino-termin
112	33	97.1	34	11	AAR07922	Human parathyroid
113	33	97.1	34	18	AAW17955	Human parathyroid
114	33	97.1	34	19	AAW48392	Human parathyroid
115	33	97.1	34	21	AAV98010	Human amino-termin
116	33	97.1	34	21	AAV98011	Human amino-termin
117	33	97.1	34	21	AAV98014	Human amino-termin
118	33	97.1	34	22	AAB96929	Human parathyroid
119	33	97.1	34	22	AAB91113	Parathyroid hormon
120	33	97.1	34	23	AAE23728	Human parathyroid
121	33	97.1	34	23	AAE18399	Human PTH peptide
122	33	97.1	34	23	AAU73032	Parathyroid hormon
123	33	97.1	36	12	AAR15842	Human parathyroid
124	33	97.1	36	13	AAR23995	Human paprthyroid
125	33	97.1	36	15	AAR58254	[4-aminosalicylic
126	33	97.1	36	15	AAR58255	[TMSA1]-hPTH(1-36)
127	33	97.1	36	15	AAR58256	[Phe1]-hPTH(1-36)-
128	33	97.1	36	15	AAR58257	[Propargylglycin1]
129	33	97.1	36	15	AAR58262	[Ala1]-hPTH(1-36)-
130	33	97.1	36	15	AAR58243	Propargyl-[A1]-hPT
131	33	97.1	36	15	AAR58247	[Hyp1]-hPTH(1-36)-
132	33	97.1	36	15	AAR58248	N-Dimethyl-[Ala1]-
133	33	97.1	36	15	AAR58250	[Lys(For)1]-hPTH(1
134	33	97.1	36	15	AAR58251	[D-glyceric acid1]
135	33	97.1	36	15	AAR58252	[Asn1]-hPTH(1-36)-
136	33	97.1	36	15	AAR58253	[4-aminobenzoic ac
137	33	97.1	36	15	AAR58191	[Ala34]-hPTH(1-36)
138	33	97.1	36	15	AAR58169	[D-Pro1]-hPTH(1-36
139	33	97.1	36	15	AAR58170	[Nva1]-hPTH(1-36)-
140	33	97.1	36	15	AAR58172	[Indole-2-carboxyl
141	33	97.1	36	15	AAR58173	[Indole-3-carboxyl
142	33	97.1	36	15	AAR58174	[Pyridine-3-carbox
143	33	97.1	36	15	AAR58175	[Pyridine-2-carbox
144	33	97.1	36	15	AAR58176	[Hexahydropyridazi
145	33	97.1	36	15	AAR58177	[Morpholine-2-carb
146	33	97.1	36	15	AAR58178	[Pro1]-hPTH(1-36)-
147	33	97.1	36	15	AAR58179	[Leu1]-hPTH(1-36)-
148	33	97.1	36	15	AAR58180	[Ile1]-hPTH(1-36)-
149	33	97.1	36	15	AAR58026	N-alpha-methyl[Ala
150	33	97.1	36	15	AAR58168	[1-amino-cyclopent
151	33	97.1	37	23	AAU73027	Parathyroid hormon
152	33	97.1	38	3	AAP20248	Parathyroid hormon
153	33	97.1	38	15	AAR58019	N-alpha-methyl[Ala
154	33	97.1	38	15	AAR58022	[Ile1]-hPTH(1-38)-
155	33	97.1	38	15	AAR58028	[Thr1]-hPTH(1-38)-
156	33	97.1	38	15	AAR58029	[Leu1]-hPTH(1-38)-
157	33	97.1	38	15	AAR58030	[Abu1 or Gabal]-hP
158	32	94.1	33	21	AAV98012	Human amino-termin
159	32	94.1	33	21	AAV98015	Human amino-termin
160	32	94.1	34	15	AAR58181	[Thr33, Ala34]-hPT
161	32	94.1	34	19	AAW42614	Human parathyroid
162	32	94.1	34	22	AAB61638	Peptide #1 that ca
163	32	94.1	36	15	AAR58259	[aBU2]-hPTH(1-36)-
164	32	94.1	36	15	AAR58261	[Tert.Leu]-hPTH(1-



165	32	94.1	36	15	AAR58236	[Ala33]-hPTH(1-36)
166	32	94.1	38	15	AAR58023	[Ala1, Abu2 or Nva2
167	32	94.1	38	15	AAR58024	[Ala1, Ile2]-hPTH(1
168	32	94.1	38	15	AAR58162	[Arg33]-hPTH(1-38)
169	32	94.1	38	15	AAR58163	[Pro33]-hPTH(1-38)
170	32	94.1	38	15	AAR58164	[Asp33]-hPTH(1-38)
171	32	94.1	38	15	AAR58165	[Ile33]-hPTH(1-38)
172	32	94.1	38	15	AAR58166	[Lys33]-hPTH(1-38)
173	32	94.1	38	15	AAR58075	[Ser33]-hPTH(1-38)
174	32	94.1	38	15	AAR58076	[Thr33]-hPTH(1-38)
175	32	94.1	38	15	AAR58077	[Leu33]-hPTH(1-38)
176	32	94.1	38	15	AAR58078	[Gly33]-hPTH(1-38)
177	32	94.1	38	15	AAR58084	[Gln33]-hPTH(1-38)
178	31	91.2	31	19	AAW42059	Human parathyroid
179	31	91.2	31	19	AAW42051	Human parathyroid
180	31	91.2	31	20	AAV02578	N-terminal 31 resi
181	31	91.2	31	22	AAB81080	Human parathyroid
182	31	91.2	31	22	AAB91097	Parathyroid hormon
183	31	91.2	31	23	AAE23720	Human parathyroid
184	31	91.2	31	23	AAU73039	Parathyroid hormon
185	31	91.2	32	5	AAP40427	Parathyroid antago
186	31	91.2	32	23	AAU73176	Parathyroid hormon
187	31	91.2	34	14	AAR41550	[D-Ala3]hPTH (1-34
188	31	91.2	34	15	AAR58232	[Lys32]-hPTH(1-34)
189	31	91.2	34	18	AAW17957	Human parathyroid
190	31	91.2	36	15	AAR58234	[Ala32]-hPTH(1-36)
191	31	91.2	36	15	AAR58197	[Ala3]-hPTH(1-36)-
192	30	88.2	30	17	AAR88832	Human parathyroid
193	30	88.2	30	23	AAE23752	Human parathyroid
194	30	88.2	30	23	AAU73051	Parathyroid hormon
195	30	88.2	31	5	AAP40760	Human parathyroid
196	30	88.2	31	23	AAU73177	Parathyroid hormon
197	30	88.2	32	23	AAE23735	Human parathyroid
198	30	88.2	34	18	AAW17948	Human parathyroid
199	30	88.2	34	18	AAW17968	Human parathyroid
200	30	88.2	34	19	AAW67283	Parathyroid hormon
201	30	88.2	36	15	AAR58231	[Ala31]-hPTH(1-36)
202	30	88.2	38	15	AAR58167	[Ile31, Arg33]-hPTH(
203	29	85.3	29	17	AAR88836	Human parathyroid
204	29	85.3	29	23	AAU73063	Parathyroid hormon
205	29	85.3	30	23	AAU73055	Parathyroid hormon
206	29	85.3	30	23	AAU73178	Parathyroid hormon
207	29	85.3	34	19	AAW67290	Parathyroid hormon
208	29	85.3	36	15	AAR58229	[Ala30]-hPTH(1-36)
209	29	85.3	38	15	AAR58161	[Pro3, Thr33]-hPTH(
210	28	82.4	28	13	AAR22064	Modified hPTH(7-34
211	28	82.4	28	17	AAR88837	Human parathyroid
212	28	82.4	28	21	AAV98052	Human parathyroid
213	28	82.4	28	23	AAE23734	Human parathyroid
214	28	82.4	28	23	AAU73044	Parathyroid hormon
215	28	82.4	28	23	AAU73064	Parathyroid hormon
216	28	82.4	29	12	AAR11731	Adenine-rich PTH-(
217	28	82.4	29	23	AAU73179	Parathyroid hormon
218	28	82.4	32	21	AAB07468	Antigenic peptide
219	28	82.4	34	18	AAW01609	Parathyroid hormon
220	28	82.4	34	18	AAW01610	Parathyroid hormon
221	28	82.4	34	19	AAW67293	Parathyroid hormon

222	28	82.4	36	15	AAR58190	[Ala29]-hPTH(1-36)
223	28	82.4	38	17	AAR98958	Target peptide (PT
224	27	79.4	28	13	AAR22065	Modified [Tyr <sub>34</sub> ]h
225	27	79.4	28	21	AAAY98048	Human parathyroid
226	27	79.4	28	21	AAAY98050	Human parathyroid
227	27	79.4	34	18	AAW17943	Human parathyroid
228	27	79.4	34	18	AAW17947	Human parathyroid
229	27	79.4	34	18	AAW17951	Human parathyroid
230	27	79.4	34	19	AAW67278	Parathyroid hormon
231	27	79.4	34	19	AAW67282	Parathyroid hormon
232	27	79.4	34	19	AAW67286	Parathyroid hormon
233	27	79.4	38	15	AAR58159	[Val28]-hPTH(1-38)
234	27	79.4	38	15	AAR58160	[Ile28]-hPTH(1-38)
235	26	76.5	28	17	AAR88838	Human parathyroid
236	26	76.5	28	21	ABJ10776	Human parathyroid
237	26	76.5	28	22	AAB81074	Human parathyroid
238	26	76.5	29	17	AAR88839	Human parathyroid
239	26	76.5	29	22	AAB81075	Human parathyroid
240	26	76.5	30	17	AAR88833	Human parathyroid
241	26	76.5	30	19	AAW42052	Human parathyroid
242	26	76.5	30	23	AAU73062	Parathyroid hormon
243	26	76.5	31	19	AAW42056	Human parathyroid
244	26	76.5	31	19	AAW42057	Human parathyroid
245	26	76.5	31	19	AAW42060	Human parathyroid
246	26	76.5	31	19	AAW42062	Human parathyroid
247	26	76.5	31	19	AAW42067	Human parathyroid
248	26	76.5	31	19	AAW42049	Human parathyroid
249	26	76.5	31	19	AAW42050	Human parathyroid
250	26	76.5	31	19	AAW42053	Human parathyroid
251	26	76.5	31	23	AAU73040	Parathyroid hormon
252	26	76.5	31	23	AAU82640	Analogue of human
253	26	76.5	33	17	AAR88841	Human parathyroid
254	26	76.5	34	13	AAR22293	Human parathyroid
255	26	76.5	34	13	AAR22298	Human parathyroid
256	26	76.5	34	13	AAR22299	Human parathyroid
257	26	76.5	34	14	AAR41554	[Thr27]hPTH (1-34)
258	26	76.5	34	14	AAR41555	[Asn27]hPTH (1-34)
259	26	76.5	34	14	AAR41558	[Ser27]hPTH (1-34)
260	26	76.5	34	14	AAR41559	[Gly27]hPTH (1-34)
261	26	76.5	34	14	AAR41560	[His27]hPTH (1-34)
262	26	76.5	34	15	AAR49697	Sequence of varian
263	26	76.5	34	15	AAR49698	Sequence of varian
264	26	76.5	34	17	AAR88829	Human parathyroid
265	26	76.5	34	17	AAR88834	Human parathyroid
266	26	76.5	34	18	AAW17969	Human parathyroid
267	26	76.5	34	19	AAW67292	Parathyroid hormon
268	26	76.5	34	19	AAW67297	Parathyroid hormon
269	26	76.5	34	19	AAW67299	Parathyroid hormon
270	26	76.5	34	19	AAW42054	Human parathyroid
271	26	76.5	34	19	AAW42055	Human parathyroid
272	26	76.5	34	21	ABJ10706	Human parathyroid
273	26	76.5	34	21	ABJ10714	Human parathyroid
274	26	76.5	34	21	ABJ10717	Human parathyroid
275	26	76.5	34	21	ABJ10719	Human parathyroid
276	26	76.5	34	21	ABJ10722	Human parathyroid
277	26	76.5	34	21	ABJ10724	Human parathyroid
278	26	76.5	34	21	ABJ10727	Human parathyroid

279	26	76.5	34	21	ABJ10729	Human parathyroid
280	26	76.5	34	21	ABJ10730	Human parathyroid
281	26	76.5	34	21	ABJ10733	Human parathyroid
282	26	76.5	34	21	ABJ10736	Human parathyroid
283	26	76.5	36	15	AAR58266	[Nle8]-hPTH(1-36)-
284	26	76.5	36	15	AAR58267	[Phe8]-hPTH(1-36)-
285	26	76.5	36	15	AAR58268	[Cha8]-hPTH(1-36)-
286	26	76.5	36	15	AAR58222	[His27]-hPTH(1-36)
287	26	76.5	36	15	AAR58223	[Phe27]-hPTH(1-36)
288	26	76.5	36	15	AAR58224	[Nle27]-hPTH(1-36)
289	26	76.5	36	15	AAR58225	[Asn27]-hPTH(1-36)
290	26	76.5	36	15	AAR58226	[Ala27]-hPTH(1-36)
291	26	76.5	36	15	AAR58182	[Nva8]-hPTH(1-36)-
292	26	76.5	38	15	AAR58269	[Leu8]-hPTH(1-38)-
293	26	76.5	38	15	AAR58154	[Val27]-hPTH(1-38)
294	26	76.5	38	15	AAR58155	[Ile27]-hPTH(1-38)
295	26	76.5	38	15	AAR58156	[Leu27]-hPTH(1-38)
296	26	76.5	38	15	AAR58157	[Arg27]-hPTH(1-38)
297	26	76.5	38	15	AAR58158	[Ala27]-hPTH(1-38)
298	25	73.5	32	17	AAR88840	Human parathyroid
299	25	73.5	34	14	AAR41556	[Gln26,27]hPTH (1-
300	25	73.5	34	14	AAR41566	[Arg 26,27]hPTH (1
301	25	73.5	34	14	AAR41567	[Gln26]hPTH (1-34)
302	25	73.5	34	21	ABJ10772	Human parathyroid
303	25	73.5	34	21	ABJ10773	Human parathyroid
304	25	73.5	36	15	AAR58290	[Ala26]-hPTH(1-36)
305	25	73.5	36	15	AAR58218	[Gln26]-hPTH(1-36)
306	25	73.5	36	15	AAR58219	[Nle26]-hPTH(1-36)
307	25	73.5	38	15	AAR58153	[Arg26]-hPTH(1-38)
308	24	70.6	31	17	AAR88830	Human parathyroid
309	24	70.6	34	14	AAR34456	Human parathyroid
310	24	70.6	34	14	AAR34457	Human parathyroid
311	24	70.6	34	14	AAR41557	[Gln25,26,27]hPTH
312	24	70.6	34	17	AAW15812	[Trp(10)]-hPTH(1-3
313	24	70.6	34	18	AAW08120	Human PTH derivati
314	24	70.6	34	18	AAW08109	Human parathyroid
315	24	70.6	34	18	AAW08114	Human PTH derivati
316	24	70.6	34	18	AAW08118	Human PTH derivati
317	24	70.6	34	18	AAW08119	Human PTH derivati
318	24	70.6	36	15	AAR58287	[Phe25]-hPTH(1-36)
319	24	70.6	36	15	AAR58288	[Lys25]-hPTH(1-36)
320	24	70.6	36	15	AAR58289	[Ala25]-hPTH(1-36)
321	24	70.6	36	15	AAR58192	[Gln25]-hPTH(1-36)
322	24	70.6	36	15	AAR58201	[Ala10]-hPTH(1-36)
323	23	67.6	34	13	AAR22292	Human parathyroid
324	23	67.6	34	13	AAR22294	Human parathyroid
325	23	67.6	34	13	AAR22296	Human parathyroid
326	23	67.6	34	18	AAW08108	Human parathyroid
327	23	67.6	34	18	AAW08113	Human PTH derivati
328	23	67.6	34	18	AAW08117	Human PTH derivati
329	23	67.6	34	18	AAW17949	Human parathyroid
330	23	67.6	34	18	AAW17941	Human parathyroid
331	23	67.6	34	18	AAW17945	Human parathyroid
332	23	67.6	34	18	AAW17939	Human parathyroid
333	23	67.6	34	18	AAW17950	Human PTH analogue
334	23	67.6	34	19	AAW67274	Parathyroid hormon
335	23	67.6	34	19	AAW67276	Parathyroid hormon

336	23	67.6	34	19	AAW67280	Parathyroid hormon
337	23	67.6	34	19	AAW67284	Parathyroid hormon
338	23	67.6	34	19	AAW67285	Parathyroid hormon
339	23	67.6	34	19	AAW67288	Parathyroid hormon
340	23	67.6	34	19	AAW67289	Parathyroid hormon
341	23	67.6	34	19	AAW67294	Parathyroid hormon
342	23	67.6	34	19	AAW67295	Parathyroid hormon
343	23	67.6	34	19	AAW67296	Parathyroid hormon
344	23	67.6	34	19	AAW67303	Parathyroid hormon
345	23	67.6	34	21	ABJ10713	Human parathyroid
346	23	67.6	34	21	ABJ10737	Human parathyroid
347	23	67.6	34	21	ABJ10769	Human parathyroid
348	23	67.6	34	23	AAU73029	Parathyroid hormon
349	23	67.6	34	23	AAU73030	Parathyroid hormon
350	23	67.6	35	23	AAU73173	Parathyroid hormon
351	23	67.6	36	15	AAR58271	[Ala11]-hPTH(1-36)
352	22	64.7	30	23	AAU73136	Parathyroid hormon
353	22	64.7	30	23	AAU73137	Parathyroid hormon
354	22	64.7	33	9	AAP82176	Sequence of parath
355	22	64.7	34	11	AAR08300	Human parathyroid
356	22	64.7	34	14	AAR34358	Human parathyroid
357	22	64.7	34	14	AAR34353	Human parathyroid
358	22	64.7	34	14	AAR34354	Human parathyroid
359	22	64.7	34	14	AAR34355	Human parathyroid
360	22	64.7	34	14	AAR34356	Human parathyroid
361	22	64.7	34	14	AAR34357	Human parathyroid
362	22	64.7	34	14	AAR34359	Human parathyroid
363	22	64.7	34	14	AAR34360	Human parathyroid
364	22	64.7	34	14	AAR34361	Human parathyroid
365	22	64.7	34	14	AAR34362	Human parathyroid
366	22	64.7	34	14	AAR34363	Human parathyroid
367	22	64.7	34	14	AAR34364	Human parathyroid
368	22	64.7	34	14	AAR34365	Human parathyroid
369	22	64.7	34	14	AAR34366	Human parathyroid
370	22	64.7	34	14	AAR34367	Human parathyroid
371	22	64.7	34	14	AAR34368	Human parathyroid
372	22	64.7	34	15	AAR58187	[Phe23,His25,His26
373	22	64.7	34	15	AAR58189	[F23,H25,H26,L27,I
374	22	64.7	34	18	AAW08121	Human PTH derivati
375	22	64.7	34	18	AAW08115	Human PTH derivati
376	22	64.7	34	18	AAW08116	Human PTH derivati
377	22	64.7	34	18	AAW17944	Human parathyroid
378	22	64.7	34	18	AAW17959	Human parathyroid
379	22	64.7	34	19	AAW67279	Parathyroid hormon
380	22	64.7	34	22	AAB91085	Parathyroid hormon
381	22	64.7	34	23	AAU73100	Parathyroid hormon
382	22	64.7	34	23	AAU73101	Parathyroid hormon
383	22	64.7	36	15	AAR58285	[Ala23]-hPTH(1-36)
384	22	64.7	36	15	AAR58203	[Ala12]-hPTH(1-36)
385	22	64.7	36	15	AAR58188	[Phe23]-hPTH(1-36)
386	22	64.7	38	15	AAR58089	[Arg12]-hPTH(1-38)
387	22	64.7	38	15	AAR58090	[Ser12]-hPTH(1-38)
388	21	61.8	28	13	AAR22066	Modified [D-Trp_12
389	21	61.8	30	23	AAU73138	Parathyroid hormon
390	21	61.8	30	23	AAU73139	Parathyroid hormon
391	21	61.8	31	19	AAW42063	Human parathyroid
392	21	61.8	31	19	AAW42065	Human parathyroid

393	21	61.8	31	19	AAW42066	Human parathyroid
394	21	61.8	34	11	AAR08303	Human parathyroid
395	21	61.8	34	15	AAR58193	[L8,D10,K11,T33,A3
396	21	61.8	34	15	AAR58194	[A1,H5,L8,D10,K11,
397	21	61.8	34	18	AAW08112	Human PTH derivati
398	21	61.8	34	19	AAW67305	Parathyroid hormon
399	21	61.8	34	19	AAW67302	Parathyroid hormon
400	21	61.8	34	19	AAW67304	Parathyroid hormon
401	21	61.8	34	22	AAB96893	Rat parathyroid ho
402	21	61.8	34	22	AAB96930	Rat parathyroid ho
403	21	61.8	34	23	AAU73102	Parathyroid hormon
404	21	61.8	34	23	AAU73103	Parathyroid hormon
405	21	61.8	34	23	AAU73104	Parathyroid hormon
406	21	61.8	34	23	AAU73140	Parathyroid hormon
407	21	61.8	36	15	AAR58204	[Gln13]-hPTH(1-36)
408	21	61.8	36	15	AAR58205	[His13]-hPTH(1-36)
409	21	61.8	36	15	AAR58206	[Leu13]-hPTH(1-36)
410	21	61.8	36	15	AAR58207	[Ala13]-hPTH(1-36)
411	21	61.8	36	15	AAR58217	[Ala22]-hPTH(1-36)
412	21	61.8	38	15	AAR58145	[Gly22]-hPTH(1-38)
413	21	61.8	38	15	AAR58146	[Leu22]-hPTH(1-38)
414	21	61.8	38	15	AAR58147	[His22]-hPTH(1-38)
415	21	61.8	38	15	AAR58148	[Ala22]-hPTH(1-38)
416	21	61.8	38	15	AAR58149	[Ile22]-hPTH(1-38)
417	21	61.8	38	15	AAR58150	[Val22]-hPTH(1-38)
418	21	61.8	38	15	AAR58151	[Ser22]-hPTH(1-38)
419	21	61.8	38	15	AAR58152	[Arg22]-hPTH(1-38)
420	21	61.8	38	15	AAR58091	[Cys13]-hPTH(1-38)
421	21	61.8	38	15	AAR58092	[Ile13]-hPTH(1-38)
422	21	61.8	38	15	AAR58093	[Asn13]-hPTH(1-38)
423	21	61.8	38	15	AAR58094	[Trp13]-hPTH(1-38)
424	21	61.8	38	15	AAR58095	[Asp13]-hPTH(1-38)
425	21	61.8	38	15	AAR58096	[Val13]-hPTH(1-38)
426	21	61.8	38	15	AAR58097	[Thr13]-hPTH(1-38)
427	21	61.8	38	15	AAR58098	[Ser13]-hPTH(1-38)
428	21	61.8	38	15	AAR58099	[Tyr13]-hPTH(1-38)
429	21	61.8	38	15	AAR58100	[Met13]-hPTH(1-38)
430	21	61.8	38	15	AAR58101	[Gln13]-hPTH(1-38)
431	21	61.8	38	15	AAR58102	[Leu13]-hPTH(1-38)
432	21	61.8	38	15	AAR58103	[Ala13]-hPTH(1-38)
433	21	61.8	38	15	AAR58104	[Gly13]-hPTH(1-38)
434	20	58.8	30	6	AAP50665	Human parathyroid
435	20	58.8	34	18	AAW24276	Parathyroid hormon
436	20	58.8	34	18	AAW08129	Human PTH derivati
437	20	58.8	34	22	AAB84771	Parathyroid hormon
438	20	58.8	34	22	AAB84826	Parathyroid hormon
439	20	58.8	34	22	AAB96916	Parathyroid hormon
440	20	58.8	34	22	AAB96919	Parathyroid hormon
441	20	58.8	36	15	AAR58209	[Ala14]-hPTH(1-36)
442	20	58.8	36	15	AAR58216	[Ala21]-hPTH(1-36)
443	20	58.8	38	15	AAR58037	[Ser14]-hPTH(1-38)
444	20	58.8	38	15	AAR58138	[Ala21]-hPTH(1-38)
445	20	58.8	38	15	AAR58139	[Gly21]-hPTH(1-38)
446	20	58.8	38	15	AAR58140	[Phe21]-hPTH(1-38)
447	20	58.8	38	15	AAR58141	[Leu21]-hPTH(1-38)
448	20	58.8	38	15	AAR58142	[Asn21]-hPTH(1-38)
449	20	58.8	38	15	AAR58143	[Gln21]-hPTH(1-38)

450	20	58.8	38	15	AAR58144	[Ser21]-hPTH(1-38)
451	20	58.8	38	15	AAR58105	[Val14]-hPTH(1-38)
452	20	58.8	38	15	AAR58106	[Ala14]-hPTH(1-38)
453	20	58.8	38	15	AAR58107	[Lys14]-hPTH(1-38)
454	20	58.8	38	15	AAR58108	[Arg14]-hPTH(1-38)
455	20	58.8	38	15	AAR58109	[Thr14]-hPTH(1-38)
456	20	58.8	38	15	AAR58110	[Ile14]-hPTH(1-38)
457	20	58.8	38	15	AAR58111	[Tyr14]-hPTH(1-38)
458	19	55.9	30	23	AAU73052	Parathyroid hormon
459	19	55.9	30	23	AAU73053	Parathyroid hormon
460	19	55.9	31	17	AAR88831	Human parathyroid
461	19	55.9	34	18	AAW17942	Human parathyroid
462	19	55.9	34	18	AAW17952	Human parathyroid
463	19	55.9	34	19	AAW67277	Parathyroid hormon
464	19	55.9	34	19	AAW67287	Parathyroid hormon
465	19	55.9	34	19	AAW48394	Human PTH/PTHrP hy
466	19	55.9	35	23	AAU73174	Parathyroid hormon
467	19	55.9	36	15	AAR58274	[Ala15]-hPTH(1-36)
468	19	55.9	36	15	AAR58279	[Lys20]-hPTH(1-36)
469	19	55.9	38	15	AAR58061	[Ile15]-hPTH(1-38)
470	19	55.9	38	15	AAR58137	[Phe20]-hPTH(1-38)
471	19	55.9	38	15	AAR58112	[Tyr15]-hPTH(1-38)
472	19	55.9	38	15	AAR58113	[Arg15]-hPTH(1-38)
473	19	55.9	38	15	AAR58114	[Val15]-hPTH(1-38)
474	18	52.9	28	13	AAR22058	Modified bovine PT
475	18	52.9	28	21	AAV98046	Human parathyroid
476	18	52.9	28	23	AAU73046	Parathyroid hormon
477	18	52.9	30	23	AAU73054	Parathyroid hormon
478	18	52.9	32	22	AAB91096	Parathyroid hormon
479	18	52.9	32	23	AAE23739	Bovine parathyroid
480	18	52.9	32	23	AAE18402	Bovine PTH peptide
481	18	52.9	32	23	AAU73042	Parathyroid hormon
482	18	52.9	34	11	AAR07918	Bovine parathyroid
483	18	52.9	34	11	AAR08299	Bovine parathyroid
484	18	52.9	34	13	AAR22297	Human parathyroid
485	18	52.9	34	14	AAR41551	[Thr16]hPTH (1-34)
486	18	52.9	34	14	AAR41552	[Glu16]hPTH (1-34)
487	18	52.9	34	14	AAR41553	[Lys16]hPTH (1-34)
488	18	52.9	34	14	AAR41571	[D-Lys16]hPTH (1-34)
489	18	52.9	34	14	AAR41573	[Gln16]hPTH (1-34)
490	18	52.9	34	14	AAR41574	[Ser16]hPTH (1-34)
491	18	52.9	34	14	AAR41575	[Gly16]hPTH (1-34)
492	18	52.9	34	14	AAR41576	[Lys16]hPTH (1-34)
493	18	52.9	34	17	AAR99979	Bovine parathyroid
494	18	52.9	34	18	AAW08124	Human PTH derivati
495	18	52.9	34	18	AAW08111	Human PTH derivati
496	18	52.9	34	18	AAW19995	Cyclised bovine pa
497	18	52.9	34	18	AAW20001	Cyclised bovine pa
498	18	52.9	34	18	AAW20007	Cyclised bovine pa
499	18	52.9	34	18	AAW17953	Human parathyroid
500	18	52.9	34	18	AAW17954	Human parathyroid
501	18	52.9	34	18	AAW17963	Human PTH analogue
502	18	52.9	34	19	AAW61659	Parathyroid hormon
503	18	52.9	34	19	AAW65976	Bovine parathyroid
504	18	52.9	34	19	AAW42615	Bovine parathyroid
505	18	52.9	34	20	AAW81872	Bovine PTH N-termi
506	18	52.9	34	22	AAB84775	Parathyroid hormon

507	18	52.9	34	22	AAB96922	Parathyroid hormon
508	18	52.9	34	23	AAE23738	Bovine parathyroid
509	18	52.9	34	23	AAE18394	Bovine PTH peptide
510	18	52.9	34	23	AAU73031	Parathyroid hormon
511	18	52.9	34	23	AAU73034	Parathyroid hormon
512	18	52.9	35	23	AAU73175	Parathyroid hormon
513	18	52.9	36	15	AAR58275	[Ala16]-hPTH(1-36)
514	18	52.9	36	15	AAR58214	[Ala19]-hPTH(1-36)
515	18	52.9	37	22	AAB86230	Bovine parathyroid
516	18	52.9	37	22	AAB86233	Canine parathyroid
517	18	52.9	37	23	ABB82204	Bovine parathyroid
518	18	52.9	38	15	AAR58036	[Gln16]-hPTH(1-38)
519	18	52.9	38	15	AAR58136	[Arg19]-hPTH(1-38)
520	18	52.9	38	15	AAR58115	[Lys16]-hPTH(1-38)
521	18	52.9	38	15	AAR58116	[Ser16]-hPTH(1-38)
522	18	52.9	38	15	AAR58117	[Leu16]-hPTH(1-38)
523	18	52.9	38	15	AAR58118	[Ala16]-hPTH(1-38)
524	18	52.9	38	15	AAR58119	[Gly16]-hPTH(1-38)
525	18	52.9	38	15	AAR58123	[Ser19]-hPTH(1-38)
526	18	52.9	38	15	AAR58124	[Lys19]-hPTH(1-38)
527	18	52.9	38	15	AAR58125	[Leu19]-hPTH(1-38)
528	18	52.9	38	15	AAR58126	[Ala19]-hPTH(1-38)
529	18	52.9	38	15	AAR58127	[Tyr19]-hPTH(1-38)
530	18	52.9	38	15	AAR58128	[Met19]-hPTH(1-38)
531	18	52.9	38	15	AAR58129	[His19]-hPTH(1-38)
532	18	52.9	38	15	AAR58130	[Val19]-hPTH(1-38)
533	18	52.9	38	15	AAR58131	[Gly19]-hPTH(1-38)
534	18	52.9	38	15	AAR58132	[Pro19]-hPTH(1-38)
535	18	52.9	38	15	AAR58133	[Asp19]-hPTH(1-38)
536	18	52.9	38	15	AAR58134	[Ile19]-hPTH(1-38)
537	18	52.9	38	15	AAR58135	[Val19,Gln24]-hPTH
538	17	50.0	28	13	AAR22059	Modified [Tyr_34]b
539	17	50.0	28	13	AAR22060	Modified [D-Trp_12
540	17	50.0	28	21	AAAY98041	Human parathyroid
541	17	50.0	28	21	AAAY98042	Human parathyroid
542	17	50.0	28	21	AAAY98044	Human parathyroid
543	17	50.0	28	22	AAB91115	Parathyroid hormon
544	17	50.0	28	23	AAE18405	Bovine PTH peptide
545	17	50.0	28	23	AAU73047	Parathyroid hormon
546	17	50.0	28	23	AAU73050	Parathyroid hormon
547	17	50.0	31	5	AAP40510	Bovine parathyroid
548	17	50.0	31	21	AAAY96973	Parathyroid hormon
549	17	50.0	31	21	AAAY96974	Parathyroid hormon
550	17	50.0	34	11	AAR07921	Bovine parathyroid
551	17	50.0	34	11	AAR08302	Bovine parathyroid
552	17	50.0	34	13	AAR22291	Human parathyroid
553	17	50.0	34	14	AAR41577	[Lys16, Asp17]hPTH
554	17	50.0	34	14	AAR41578	[Lys14,15,16,17]hP
555	17	50.0	34	14	AAR41579	[Lys15,15,17]hPTH
556	17	50.0	34	14	AAR41580	[Lys16,17]hPTH (1-
557	17	50.0	34	14	AAR41581	[Arg16,17]hPTH (1-
558	17	50.0	34	14	AAR41582	[Arg15,16,17]hPTH
559	17	50.0	34	17	AAW14308	Cyclic parathyroid
560	17	50.0	34	17	AAW14309	Cyclic parathyroid
561	17	50.0	34	17	AAW14310	Cyclic parathyroid
562	17	50.0	34	17	AAW14311	Cyclic parathyroid
563	17	50.0	34	17	AAW14312	Cyclic parathyroid

564	17	50.0	34	17	AAW14313	Cyclic parathyroid
565	17	50.0	34	17	AAW14314	Cyclic parathyroid
566	17	50.0	34	17	AAW14315	Cyclic parathyroid
567	17	50.0	34	18	AAW08122	Human PTH derivati
568	17	50.0	34	18	AAW08123	Human PTH derivati
569	17	50.0	34	18	AAW17958	Human parathyroid
570	17	50.0	34	19	AAW67298	Parathyroid hormon
571	17	50.0	34	19	AAW67300	Parathyroid hormon
572	17	50.0	34	19	AAW67301	Parathyroid hormon
573	17	50.0	34	21	ABJ10742	Human parathyroid
574	17	50.0	34	22	AAB91087	Parathyroid hormon
575	17	50.0	36	15	AAR58277	[Nle18]-hPTH(1-36)
576	17	50.0	36	15	AAR58212	[Ala17]-hPTH(1-36)
577	17	50.0	36	15	AAR58183	[Gln18]-hPTH(1-36)
578	17	50.0	36	15	AAR58184	[Tyr18]-hPTH(1-36)
579	17	50.0	36	15	AAR58185	[Lys18]-hPTH(1-36)
580	17	50.0	36	15	AAR58186	[Ala18]-hPTH(1-36)
581	17	50.0	38	15	AAR58120	[Ala17]-hPTH(1-38)
582	17	50.0	38	15	AAR58121	[Met17]-hPTH(1-38)
583	17	50.0	38	15	AAR58122	[Ile17]-hPTH(1-38)
584	16	47.1	28	21	ABJ10775	Human parathyroid
585	16	47.1	28	22	AAB81078	Human parathyroid
586	16	47.1	28	23	AAU73105	Parathyroid hormon
587	16	47.1	28	23	AAU73106	Parathyroid hormon
588	16	47.1	31	22	AAB81077	Human parathyroid
589	16	47.1	34	13	AAR22295	Human parathyroid
590	16	47.1	34	15	AAR58239	Isopropyl- [Nle8,18
591	16	47.1	34	15	AAR58241	[Nle8,18,D-Asn33,D
592	16	47.1	34	17	AAW14316	Cyclic parathyroid
593	16	47.1	34	17	AAR99981	Porcine parathyroi
594	16	47.1	34	19	AAW61660	Parathyroid hormon
595	16	47.1	34	19	AAW65977	Porcine parathyroi
596	16	47.1	34	19	AAW42616	Porcine parathyroi
597	16	47.1	34	20	AAW92218	Analogue of parath
598	16	47.1	34	20	AAW92219	Analogue of parath
599	16	47.1	34	20	AAW03920	Analogue of parath
600	16	47.1	34	20	AAW03921	Analogue of parath
601	16	47.1	34	20	AAW03922	Analogue of parath
602	16	47.1	34	20	AAW03923	Analogue of parath
603	16	47.1	34	20	AAW03924	Analogue of parath
604	16	47.1	34	20	AAW03925	Analogue of parath
605	16	47.1	34	20	AAW03926	Analogue of parath
606	16	47.1	34	20	AAW03927	Analogue of parath
607	16	47.1	34	20	AAW03928	Analogue of parath
608	16	47.1	34	20	AAW03929	Analogue of parath
609	16	47.1	34	20	AAW03930	Analogue of parath
610	16	47.1	34	20	AAW03931	Analogue of parath
611	16	47.1	34	20	AAW03932	Analogue of parath
612	16	47.1	34	20	AAW03933	Analogue of parath
613	16	47.1	34	20	AAW92236	Analogue of parath
614	16	47.1	34	20	AAW92237	Analogue of parath
615	16	47.1	34	20	AAW92238	Analogue of parath
616	16	47.1	34	20	AAW92239	Analogue of parath
617	16	47.1	34	20	AAW92240	Analogue of parath
618	16	47.1	34	20	AAW92241	Analogue of parath
619	16	47.1	34	20	AAW92242	Analogue of parath
620	16	47.1	34	20	AAW92243	Analogue of parath



621	16	47.1	34	20	AAW92244	Analogue of parath
622	16	47.1	34	20	AAW92245	Analogue of parath
623	16	47.1	34	20	AAW92246	Analogue of parath
624	16	47.1	34	20	AAW92247	Analogue of parath
625	16	47.1	34	20	AAW92248	Analogue of parath
626	16	47.1	34	20	AAW92249	Analogue of parath
627	16	47.1	34	20	AAW92250	Analogue of parath
628	16	47.1	34	20	AAW92250	Analogue of parath
629	16	47.1	34	20	AAW92220	Analogue of parath
630	16	47.1	34	20	AAW92221	Analogue of parath
631	16	47.1	34	20	AAW92222	Analogue of parath
632	16	47.1	34	20	AAW92223	Analogue of parath
633	16	47.1	34	20	AAW92224	Analogue of parath
634	16	47.1	34	20	AAW92225	Analogue of parath
635	16	47.1	34	20	AAW92226	Analogue of parath
636	16	47.1	34	20	AAW92227	Analogue of parath
637	16	47.1	34	20	AAW92228	Analogue of parath
638	16	47.1	34	20	AAW92229	Analogue of parath
639	16	47.1	34	20	AAW92230	Analogue of parath
640	16	47.1	34	20	AAW92231	Analogue of parath
641	16	47.1	34	20	AAW92232	Analogue of parath
642	16	47.1	34	20	AAW92233	Analogue of parath
643	16	47.1	34	20	AAW92234	Analogue of parath
644	16	47.1	34	20	AAW92235	Analogue of parath
645	16	47.1	34	20	AAW92235	Analogue of parath
646	16	47.1	34	20	AAW92204	Analogue of parath
647	16	47.1	34	20	AAW92204	Analogue of parath
648	16	47.1	34	20	AAW92205	Analogue of parath
649	16	47.1	34	20	AAW92207	Analogue of parath
650	16	47.1	34	20	AAW92208	Analogue of parath
651	16	47.1	34	20	AAW92209	Analogue of parath
652	16	47.1	34	20	AAW92210	Analogue of parath
653	16	47.1	34	20	AAW92211	Analogue of parath
654	16	47.1	34	20	AAW92212	Analogue of parath
655	16	47.1	34	20	AAW92213	Analogue of parath
656	16	47.1	34	20	AAW92214	Analogue of parath
657	16	47.1	34	20	AAW92215	Analogue of parath
658	16	47.1	34	20	AAW92216	Analogue of parath
659	16	47.1	34	20	AAW92217	Analogue of parath
660	16	47.1	34	20	AAW92206	Analogue of parath
661	16	47.1	34	20	AAW92203	Analogue of parath
662	16	47.1	34	20	AAW92203	Analogue of parath
663	16	47.1	34	20	AAW92203	Analogue of parath
664	16	47.1	34	20	AAW92203	Analogue of parath
665	16	47.1	34	20	AAW92203	Analogue of parath
666	16	47.1	34	20	AAW92203	Analogue of parath
667	16	47.1	34	20	AAW92203	Analogue of parath
668	16	47.1	34	20	AAW92203	Analogue of parath
669	16	47.1	34	20	AAW92203	Analogue of parath
670	16	47.1	34	20	AAW92203	Analogue of parath
671	16	47.1	34	20	AAW92203	Analogue of parath
672	16	47.1	34	20	AAW92203	Analogue of parath
673	16	47.1	34	20	AAW92203	Analogue of parath
674	16	47.1	34	20	AAW92203	Analogue of parath
675	16	47.1	34	20	AAW92203	Analogue of parath
676	16	47.1	34	20	AAW92203	Analogue of parath
677	16	47.1	34	20	AAW92203	Analogue of parath

678	16	47.1	34	20	AAW03952	Analogue of parath
679	16	47.1	34	20	AAW03953	Analogue of parath
680	16	47.1	34	20	AAW03954	Analogue of parath
681	16	47.1	34	20	AAW03955	Analogue of parath
682	16	47.1	34	20	AAW03956	Analogue of parath
683	16	47.1	34	20	AAW92198	Analogue of parath
684	16	47.1	34	20	AAW92199	Analogue of parath
685	16	47.1	34	20	AAW92200	Analogue of parath
686	16	47.1	34	20	AAW92201	Analogue of parath
687	16	47.1	34	20	AAW92202	Analogue of parath
688	16	47.1	34	20	AAW92183	Analogue of parath
689	16	47.1	34	20	AAW92184	Analogue of parath
690	16	47.1	34	20	AAW92185	Analogue of parath
691	16	47.1	34	20	AAW92186	Analogue of parath
692	16	47.1	34	20	AAW92187	Analogue of parath
693	16	47.1	34	20	AAW92167	Analogue of parath
694	16	47.1	34	20	AAW92188	Analogue of parath
695	16	47.1	34	20	AAW92189	Analogue of parath
696	16	47.1	34	20	AAW92190	Analogue of parath
697	16	47.1	34	20	AAW92191	Analogue of parath
698	16	47.1	34	20	AAW92192	Analogue of parath
699	16	47.1	34	20	AAW92193	Analogue of parath
700	16	47.1	34	20	AAW92194	Analogue of parath
701	16	47.1	34	20	AAW92195	Analogue of parath
702	16	47.1	34	20	AAW92196	Analogue of parath
703	16	47.1	34	20	AAW92197	Analogue of parath
704	16	47.1	34	20	AAW92166	Analogue of parath
705	16	47.1	34	20	AAW92168	Analogue of parath
706	16	47.1	34	20	AAW92169	Analogue of parath
707	16	47.1	34	20	AAW92170	Analogue of parath
708	16	47.1	34	20	AAW92171	Analogue of parath
709	16	47.1	34	20	AAW92172	Analogue of parath
710	16	47.1	34	20	AAW92173	Analogue of parath
711	16	47.1	34	20	AAW92174	Analogue of parath
712	16	47.1	34	20	AAW92175	Analogue of parath
713	16	47.1	34	20	AAW92176	Analogue of parath
714	16	47.1	34	20	AAW92177	Analogue of parath
715	16	47.1	34	20	AAW92178	Analogue of parath
716	16	47.1	34	20	AAW92179	Analogue of parath
717	16	47.1	34	20	AAW92180	Analogue of parath
718	16	47.1	34	20	AAW92181	Analogue of parath
719	16	47.1	34	20	AAW92182	Analogue of parath
720	16	47.1	34	20	AAW92152	Analogue of parath
721	16	47.1	34	20	AAW92150	Analogue of parath
722	16	47.1	34	20	AAW92151	Analogue of parath
723	16	47.1	34	20	AAW92153	Analogue of parath
724	16	47.1	34	20	AAW92154	Analogue of parath
725	16	47.1	34	20	AAW92155	Analogue of parath
726	16	47.1	34	20	AAW92156	Analogue of parath
727	16	47.1	34	20	AAW92157	Analogue of parath
728	16	47.1	34	20	AAW92158	Analogue of parath
729	16	47.1	34	20	AAW92159	Analogue of parath
730	16	47.1	34	20	AAW92160	Analogue of parath
731	16	47.1	34	20	AAW92161	Analogue of parath
732	16	47.1	34	20	AAW92162	Analogue of parath
733	16	47.1	34	20	AAW92163	Analogue of parath
734	16	47.1	34	20	AAW92164	Analogue of parath

735	16	47.1	34	20	AAW92165	Analogue of parath
736	16	47.1	34	20	AAW92148	Analogue of parath
737	16	47.1	34	20	AAW92149	Analogue of parath
738	16	47.1	34	20	AAW81873	Porcine PTH N-term
739	16	47.1	34	21	ABJ10735	Human parathyroid
740	16	47.1	34	21	ABJ10739	Human parathyroid
741	16	47.1	34	21	ABJ10740	Human parathyroid
742	16	47.1	34	21	ABJ10743	Human parathyroid
743	16	47.1	34	22	AAB91084	Parathyroid hormon
744	16	47.1	34	23	AAU73036	Parathyroid hormon
745	16	47.1	35	2	AAP10140	h-PTH antigen. Sy
746	16	47.1	36	15	AAR58042	[L8,D10,K11,L18]-h
747	16	47.1	36	15	AAR58044	[L8,D10,K11,A17,L1
748	16	47.1	36	15	AAR58055	[L8,Q18]-hPTH(1-36
749	16	47.1	36	15	AAR58057	[L8,D10,A16,Q18]-h
750	16	47.1	36	15	AAR58071	[Aib3, Gln18]-hPTH
751	16	47.1	36	15	AAR55820	[L8,D10,K11,Q18]-h
752	16	47.1	36	15	AAR55824	[L8,D10,K11,A16,Q1
753	16	47.1	36	15	AAR58027	[A1,A3,L8,Q18]-hPT
754	16	47.1	36	15	AAR58031	[L8,K11,Q18]-hPTH(
755	16	47.1	36	15	AAR58072	Isopropyl-[L8,D10,
756	16	47.1	36	15	AAR58074	[L8,Y18]-hPTH(1-36
757	16	47.1	36	15	AAR58088	[1-amino-cyclopent
758	16	47.1	37	22	AAB86232	Porcine parathyroi
759	15	44.1	28	13	AAR22061	Modified [Nle_8,18
760	15	44.1	28	13	AAR22062	Modified [Nle_8,18
761	15	44.1	28	13	AAR22067	Modified [Nle_8,_1
762	15	44.1	28	13	AAR22068	Modified [Nle_8,_1
763	15	44.1	28	21	ABJ10774	Human parathyroid
764	15	44.1	28	23	AAE18404	Bovine PTH peptide
765	15	44.1	28	23	AAU73045	Parathyroid hormon
766	15	44.1	28	23	AAU73048	Parathyroid hormon
767	15	44.1	28	23	AAU73049	Parathyroid hormon
768	15	44.1	28	23	AAU73107	Parathyroid hormon
769	15	44.1	28	23	AAU73108	Parathyroid hormon
770	15	44.1	28	23	AAU73109	Parathyroid hormon
771	15	44.1	30	22	AAB91089	Parathyroid hormon
772	15	44.1	30	22	AAB91092	Parathyroid hormon
773	15	44.1	30	23	AAU73059	Parathyroid hormon
774	15	44.1	31	5	AAP40511	Bovine parathyroid
775	15	44.1	31	5	AAP40761	Human parathyroid
776	15	44.1	31	21	AAV96975	Parathyroid hormon
777	15	44.1	32	22	AAB91088	Parathyroid hormon
778	15	44.1	32	22	AAB91090	Parathyroid hormon
779	15	44.1	32	22	AAB91091	Parathyroid hormon
780	15	44.1	32	23	AAE18403	Bovine PTH peptide
781	15	44.1	32	23	AAU73041	Parathyroid hormon
782	15	44.1	32	23	AAU73043	Parathyroid hormon
783	15	44.1	34	6	AAP50517	Sequence of methio
784	15	44.1	34	11	AAR07924	Bovine parathyroid
785	15	44.1	34	11	AAR07925	Human parathyroid
786	15	44.1	34	11	AAR08305	Bovine parathyroid
787	15	44.1	34	11	AAR08306	Human parathyroid
788	15	44.1	34	14	AAR41561	[Lys16, Gln27]hPTH
789	15	44.1	34	14	AAR41562	[Orn16, Gln27]hPTH
790	15	44.1	34	14	AAR41563	[Hci16, Gln27]hPTH
791	15	44.1	34	14	AAR41564	[Asp16, Gln27]hPTH

792	15	44.1	34	14	AAR41565	[Arg16, Gln27]hPTH
793	15	44.1	34	15	AAR45528	Parathyroid hormon
794	15	44.1	34	16	AAR69055	PTH analogue with
795	15	44.1	34	18	AAW13352	Truncated parathyr
796	15	44.1	34	18	AAW12651	Parathyroid hormon
797	15	44.1	34	18	AAW08130	Human PTH derivati
798	15	44.1	34	18	AAW08132	Human PTH derivati
799	15	44.1	34	18	AAW20004	Cyclised [Nle 8,18
800	15	44.1	34	18	AAW19997	Cyclised [Nle 8,18
801	15	44.1	34	18	AAW19998	Cyclised [Nle 8,18
802	15	44.1	34	18	AAW20003	Cyclised [Nle 8,18
803	15	44.1	34	18	AAW20009	Cyclised [Nle 8,18
804	15	44.1	34	18	AAW20010	Cyclised [Nle 8,18
805	15	44.1	34	18	AAW17940	Human PTH analogue
806	15	44.1	34	18	AAW17967	Human PTH analogue
807	15	44.1	34	18	AAW17970	Human PTH analogue
808	15	44.1	34	18	AAW17964	Human PTH analogue
809	15	44.1	34	18	AAW17956	Human parathyroid
810	15	44.1	34	18	AAW17962	Human PTH analogue
811	15	44.1	34	19	AAW67275	Parathyroid hormon
812	15	44.1	34	19	AAW61725	Parathyroid hormon
813	15	44.1	34	19	AAW66053	Parathyroid hormon
814	15	44.1	34	19	AAW42602	Parathyroid hormon
815	15	44.1	34	19	AAW48395	Human PTH/PTHrP hy
816	15	44.1	34	20	AAW74396	Modified parathyro
817	15	44.1	34	20	AAW81945	Synthetic PTH and
818	15	44.1	34	21	ABJ10705	Human parathyroid
819	15	44.1	34	21	ABJ10707	Human parathyroid
820	15	44.1	34	21	ABJ10708	Human parathyroid
821	15	44.1	34	21	ABJ10709	Human parathyroid
822	15	44.1	34	21	ABJ10710	Human parathyroid
823	15	44.1	34	21	ABJ10711	Human parathyroid
824	15	44.1	34	21	ABJ10715	Human parathyroid
825	15	44.1	34	21	ABJ10716	Human parathyroid
826	15	44.1	34	21	ABJ10718	Human parathyroid
827	15	44.1	34	21	ABJ10720	Human parathyroid
828	15	44.1	34	21	ABJ10721	Human parathyroid
829	15	44.1	34	21	ABJ10723	Human parathyroid
830	15	44.1	34	21	ABJ10725	Human parathyroid
831	15	44.1	34	21	ABJ10726	Human parathyroid
832	15	44.1	34	21	ABJ10728	Human parathyroid
833	15	44.1	34	21	ABJ10731	Human parathyroid
834	15	44.1	34	21	ABJ10732	Human parathyroid
835	15	44.1	34	21	ABJ10734	Human parathyroid
836	15	44.1	34	21	ABJ10738	Human parathyroid
837	15	44.1	34	21	ABJ10741	Human parathyroid
838	15	44.1	34	21	ABJ10744	Human parathyroid
839	15	44.1	34	21	ABJ10745	Human parathyroid
840	15	44.1	34	21	ABJ10746	Human parathyroid
841	15	44.1	34	21	ABJ10747	Human parathyroid
842	15	44.1	34	21	ABJ10748	Human parathyroid
843	15	44.1	34	21	ABJ10749	Human parathyroid
844	15	44.1	34	21	ABJ10750	Human parathyroid
845	15	44.1	34	21	ABJ10751	Human parathyroid
846	15	44.1	34	21	ABJ10752	Human parathyroid
847	15	44.1	34	21	ABJ10753	Human parathyroid
848	15	44.1	34	21	ABJ10754	Human parathyroid

849	15	44.1	34	21	ABJ10755	Human parathyroid
850	15	44.1	34	21	ABJ10756	Human parathyroid
851	15	44.1	34	21	ABJ10761	Human parathyroid
852	15	44.1	34	21	ABJ10762	Human parathyroid
853	15	44.1	34	21	ABJ10763	Human parathyroid
854	15	44.1	34	21	ABJ10764	Human parathyroid
855	15	44.1	34	21	ABJ10765	Human parathyroid
856	15	44.1	34	21	ABJ10766	Human parathyroid
857	15	44.1	34	21	ABJ10767	Human parathyroid
858	15	44.1	34	21	ABJ10768	Human parathyroid
859	15	44.1	34	21	ABJ10770	Human parathyroid
860	15	44.1	34	21	ABJ10771	Human parathyroid
861	15	44.1	34	21	ABJ10777	Human parathyroid
862	15	44.1	34	23	AAE18396	Bovine PTH peptide
863	15	44.1	34	23	AAE18397	Human PTH peptide
864	15	44.1	34	23	AAU73033	Parathyroid hormon
865	15	44.1	34	23	AAU73035	Parathyroid hormon
866	15	44.1	35	16	AAR74518	Parathyroid hormon
867	15	44.1	35	16	AAR74519	Parathyroid hormon
868	15	44.1	35	16	AAR74520	Parathyroid hormon
869	15	44.1	35	16	AAR74527	Human parathyroid
870	15	44.1	35	16	AAR74464	Parathyroid hormon
871	15	44.1	35	16	AAR74465	Parathyroid hormon
872	15	44.1	35	16	AAR74466	Parathyroid hormon
873	15	44.1	35	16	AAR74467	Parathyroid hormon
874	15	44.1	35	16	AAR74468	Parathyroid hormon
875	15	44.1	35	16	AAR74469	Parathyroid hormon
876	15	44.1	35	16	AAR74470	Parathyroid hormon
877	15	44.1	35	16	AAR74471	Parathyroid hormon
878	15	44.1	35	16	AAR74472	Parathyroid hormon
879	15	44.1	35	16	AAR74473	Parathyroid hormon
880	15	44.1	35	16	AAR74474	Parathyroid hormon
881	15	44.1	35	16	AAR74475	Parathyroid hormon
882	15	44.1	35	16	AAR74476	Parathyroid hormon
883	15	44.1	35	16	AAR74477	Parathyroid hormon
884	15	44.1	35	16	AAR74478	Parathyroid hormon
885	15	44.1	35	16	AAR74479	Parathyroid hormon
886	15	44.1	35	16	AAR74448	Parathyroid hormon
887	15	44.1	35	16	AAR74449	Parathyroid hormon
888	15	44.1	35	16	AAR74450	Parathyroid hormon
889	15	44.1	35	16	AAR74451	Parathyroid hormon
890	15	44.1	35	16	AAR74452	Parathyroid hormon
891	15	44.1	35	16	AAR74453	Parathyroid hormon
892	15	44.1	35	16	AAR74454	Parathyroid hormon
893	15	44.1	35	16	AAR74455	Parathyroid hormon
894	15	44.1	35	16	AAR74456	Parathyroid hormon
895	15	44.1	35	16	AAR74457	Parathyroid hormon
896	15	44.1	35	16	AAR74458	Parathyroid hormon
897	15	44.1	35	16	AAR74459	Parathyroid hormon
898	15	44.1	35	16	AAR74460	Parathyroid hormon
899	15	44.1	35	16	AAR74461	Parathyroid hormon
900	15	44.1	35	16	AAR74462	Parathyroid hormon
901	15	44.1	35	16	AAR74463	Parathyroid hormon
902	15	44.1	35	16	AAR74432	Parathyroid hormon
903	15	44.1	35	16	AAR74433	Parathyroid hormon
904	15	44.1	35	16	AAR74434	Parathyroid hormon
905	15	44.1	35	16	AAR74435	Parathyroid hormon

906	15	44.1	35	16	AAR74436	Parathyroid hormon
907	15	44.1	35	16	AAR74437	Parathyroid hormon
908	15	44.1	35	16	AAR74438	Parathyroid hormon
909	15	44.1	35	16	AAR74439	Parathyroid hormon
910	15	44.1	35	16	AAR74440	Parathyroid hormon
911	15	44.1	35	16	AAR74441	Parathyroid hormon
912	15	44.1	35	16	AAR74442	Parathyroid hormon
913	15	44.1	35	16	AAR74443	Parathyroid hormon
914	15	44.1	35	16	AAR74444	Parathyroid hormon
915	15	44.1	35	16	AAR74445	Parathyroid hormon
916	15	44.1	35	16	AAR74446	Parathyroid hormon
917	15	44.1	35	16	AAR74447	Parathyroid hormon
918	15	44.1	35	16	AAR74429	Parathyroid hormon
919	15	44.1	35	16	AAR74430	Parathyroid hormon
920	15	44.1	35	16	AAR74431	Parathyroid hormon
921	15	44.1	35	16	AAR74398	Parathyroid hormon
922	15	44.1	35	16	AAR74399	Parathyroid hormon
923	15	44.1	35	16	AAR74400	Parathyroid hormon
924	15	44.1	35	16	AAR74394	Parathyroid hormon
925	15	44.1	35	16	AAR74395	Parathyroid hormon
926	15	44.1	35	16	AAR74396	Parathyroid hormon
927	15	44.1	35	16	AAR74397	Parathyroid hormon
928	15	44.1	36	15	AAR58041	[L8,D10,K11,S14,I1
929	15	44.1	36	15	AAR58043	[L8,Q16,D17,L18,R1
930	15	44.1	36	15	AAR58046	[L8,A16,D17,L18,A1
931	15	44.1	36	15	AAR58047	[L8,D10,A16,D17,L1
932	15	44.1	36	15	AAR58050	[L8,A16,D17,Q18,A1
933	15	44.1	36	15	AAR58051	[L8,A16,A17,Q18,A1
934	15	44.1	36	15	AAR58052	[L8,A17,Q18,A19]-h
935	15	44.1	36	15	AAR58067	[L8,A16,A17,A18,A1
936	15	44.1	36	15	AAR58069	Isopropyl- [L8,K(Is
937	15	44.1	36	15	AAR58070	Isopropyl- [L8,K(Is
938	15	44.1	36	15	AAR55822	[L8,D10,K11,A16,Q1
939	15	44.1	36	15	AAR55825	[L8,A16,Q18,A19]-h
940	15	44.1	36	15	AAR58086	[1-amino-cyclopent
941	14	41.2	28	23	AAU73066	Parathyroid hormon
942	14	41.2	30	23	AAU73057	Parathyroid hormon
943	14	41.2	30	23	AAU73060	Parathyroid hormon
944	14	41.2	33	17	AAW15814	[Leu(8),Trp(10),Al
945	14	41.2	34	9	AAP82177	Sequence of parath
946	14	41.2	34	11	AAR07917	Rat parathyroid ho
947	14	41.2	34	11	AAR07920	Rat parathyroid ho
948	14	41.2	34	14	AAR41568	[Lys15,16 His27]hP
949	14	41.2	34	14	AAR41569	[Lys15, His27]hPTH
950	14	41.2	34	14	AAR41572	[Lys15,16,17, His2
951	14	41.2	34	15	AAR55817	[L8,Q18,T33,A34]-h
952	14	41.2	34	15	AAR55819	[L8,A16,Q18,T33,A3
953	14	41.2	34	15	AAR55821	[L8,D10,K11,Q18,T3
954	14	41.2	34	15	AAR55823	[L8,D10,K11,A16,Q1
955	14	41.2	34	15	AAR58021	[L8,D10,A16,Q18,T3
956	14	41.2	34	15	AAR58034	Isopropyl- [L8,K(Is
957	14	41.2	34	16	AAR62432	Accelerator peptid
958	14	41.2	34	17	AAW15813	[Leu(8),Trp(10),Al
959	14	41.2	34	17	AAW15815	[Leu(8),Trp(10),DL
960	14	41.2	34	17	AAW15828	N-alpha-acylated [
961	14	41.2	34	17	AAR99980	Rat parathyroid ho
962	14	41.2	34	18	AAW19996	Cyclised rat parat

963	14	41.2	34	18	AAW20002	Cyclised rat parat
964	14	41.2	34	18	AAW20008	Cyclised rat parat
965	14	41.2	34	18	AAW17960	Human PTH analogue
966	14	41.2	34	19	AAW48398	Human PTH/PTHrP hy
967	14	41.2	34	20	AAV02587	Parathyroid hormon
968	14	41.2	34	21	ABJ10757	Human parathyroid
969	14	41.2	34	22	AAB84777	Native human parat
970	14	41.2	34	22	AAB96897	Rat parathyroid ho
971	14	41.2	34	22	AAB91100	Parathyroid hormon
972	14	41.2	34	23	AAU73037	Parathyroid hormon
973	14	41.2	34	24	ABP71489	Parathyroid hormon
974	14	41.2	34	24	ABP71499	Rat parathyroid ho
975	14	41.2	35	16	AAR74515	Parathyroid hormon
976	14	41.2	35	16	AAR74516	Parathyroid hormon
977	14	41.2	35	16	AAR74517	Parathyroid hormon
978	14	41.2	35	16	AAR74480	Parathyroid hormon
979	14	41.2	35	16	AAR74401	Parathyroid hormon
980	14	41.2	35	16	AAR74409	Parathyroid hormon
981	14	41.2	35	16	AAR74412	Parathyroid hormon
982	14	41.2	37	22	AAB86231	Rat parathyroid ho
983	13	38.2	32	22	AAB84835	Parathyroid hormon
984	13	38.2	32	22	AAB96906	Parathyroid hormon
985	13	38.2	34	15	AAR58195	[S14,I15,Q16,D17,L
986	13	38.2	34	15	AAR58045	[L8,Q16,D17,L18,R1
987	13	38.2	34	15	AAR58049	[L8,D10,K11,Q16,D1
988	13	38.2	34	15	AAR58056	[L8,D10,K11,A16,Q1
989	13	38.2	34	15	AAR58058	[L8,D10,K11,A16,Q1
990	13	38.2	34	15	AAR55818	[L8,A16,Q18,A19,T3
991	13	38.2	34	18	AAW08131	Human PTH derivati
992	13	38.2	34	21	ABJ10758	Human parathyroid
993	13	38.2	34	22	AAB84828	Parathyroid hormon
994	13	38.2	34	22	AAB96921	Parathyroid hormon
995	13	38.2	35	16	AAR74512	Parathyroid hormon
996	13	38.2	35	16	AAR74513	Parathyroid hormon
997	13	38.2	35	16	AAR74514	Parathyroid hormon
998	13	38.2	35	16	AAR74511	Parathyroid hormon
999	13	38.2	35	16	AAR74481	Parathyroid hormon
1000	13	38.2	35	16	AAR74482	Parathyroid hormon

# ALIGNMENTS

## RESULT 1

AAP30022

ID AAP30022 standard; peptide; 34 AA.

XX

AC AAP30022;

XX

DT 25-MAR-2003 (updated)

DT 01-SEP-1992 (first entry)

XX

DE Human parathyroid-(1-34) amide.

XX

KW PTH; parathyroid gland; antibodies.

XX

OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Modified-site 34  
 FT /note= "amidated"  
 XX  
 PN JP58096052-A.  
 XX  
 PD 07-JUN-1983.  
 XX  
 PF 30-NOV-1983; 83JP-0193212.  
 XX  
 PR 31-MAR-1981; 81JP-0048887.  
 XX  
 PA (TOXN ) TOYO JOZO KK.  
 XX  
 DR WPI; 1983-709291/28.  
 XX  
 PT High activity human parathyroid hormone amide prodn. - by  
 PT condensing protected aminoacid(s) and/or peptide(s) useful for  
 PT lowering parathyroid gland function  
 XX  
 PS Claim 1; Page 1; 20pp; Japanese.  
 XX  
 CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by  
 CC the following steps: Firstly the carboxy gp. at the C-terminal  
 CC phenylalanine was converted into its amide form. The protected  
 CC individual amino acids were condensed, in order, by liquid phase  
 CC synthesis. The protecting groups were removed from the N-terminal  
 CC amino gp. and other functional gps. by acidolysis, and the  
 CC resulting hPTH(1-34)-amide purified by gel filtration  
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by  
 CC column chromatography with carboxymethyl cellulose or ion exchange  
 CC resin. The peptide amide is useful in lowering the activity of the  
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of  
 CC parathyroid gland function.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 2

AAP50377  
 ID AAP50377 standard; peptide; 34 AA.  
 XX  
 AC AAP50377;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 08-MAR-1992 (first entry)  
 XX



DE [Met(O)8,18]hPTH-(1-34).  
 XX  
 KW Human parathyroid hormone; calcium regulation.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 8  
 FT /label= oxidised methionine  
 FT Modified-site 18  
 FT /label= oxidised methionine  
 XX  
 PN JP59204159-A.  
 XX  
 PD 19-NOV-1984.  
 XX  
 PF 28-APR-1983; 83JP-0075607.  
 XX  
 PR 28-APR-1983; 83JP-0075607.  
 XX  
 PA (TOXN ) TOYO JOZO KK.  
 XX  
 DR WPI; 1985-003560/01.  
 XX  
 PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in  
 PT blood and decreases level in urine.  
 XX  
 PS Claim 1; Page 1; 3pp; Japanese.  
 XX  
 CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,  
 CC decreases Ca in urine and increases P in urine by increasing cAMP in  
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The  
 CC modified derivative only has the effect of lowering Ca levels in  
 CC urine and can be used when only this particular effect is required.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct DR field.)  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 3

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone  
DE obtainable from a human or animal.

XX

KW Osteoporosis therapy.

XX

OS Homo sapiens/animal.

XX

PN EP197514-A.

XX

PD 15-OCT-1986.

XX

PF 03-APR-1986; 86EP-0104562.

XX

PR 04-APR-1985; 85US-0720018.

PR 05-DEC-1986; 86US-0939308.

PR 21-MAY-1987; 87US-0052383.

XX

PA (GEHO ) GEN HOSPITAL CORP.

XX

PI Potts JT, Neer RM, Slovik DM;

XX

DR WPI; 1986-273437/42.

XX

PT Compsn. and kits for increasing bone mass in osteoporosis -

PT contg. parathyroid hormone or fragment with hydroxylated

PT vitamin/D cpd. or calcium salt

XX

PS Claim 4; Page 24; 26pp; English.

XX

CC The peptide is used in a pharmaceutical compsn. together with a  
CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.  
CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-  
CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-  
CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ      Sequence      34 AA;

Query Match 100.0%; Score 34; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHN LGKHLNSMERVEWLRKKLQDVHNF 34

\_\_\_\_\_

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLODVHNF 34

## RESULT 4

AAR07919

ID AAR07919 standard; protein; 34 AA.

XX

AC AAR07919;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US4968669-A.  
 XX  
 PD 06-NOV-1990.  
 XX  
 PF 21-APR-1989; 89US-0341597.  
 XX  
 PR 21-APR-1989; 89US-0341597.  
 PR 09-MAY-1988; 88US-0191512.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Rosenblatt M, Chorev M;  
 XX  
 DR WPI; 1990-354642/47.  
 XX  
 PT New para:thyroid hormone analogues - which inhibit hormone  
 PT activity by binding receptors while not producing second  
 PT messenger molecules  
 XX  
 PS Claim 1; Column 8; 6pp; English.  
 XX  
 CC Peptide analogues have high affinity for PTH cell surface receptors,  
 CC but do not stimulate production of secondary messenger molecules.  
 CC They may be used in inhibition of PTH action, and in diagnosis and  
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.  
 CC Analogues may also be used in treatment of tumours and other cells  
 CC overproducing peptide hormone-like substances, and immune diseases  
 CC eg. allergic inflammation and hyperactive lymphocytes.  
 CC Naturally occuring PTH levels may also be measured in vitro.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 11; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 5

AAR22283

ID AAR22283 standard; peptide; 34 AA.

XX

AC AAR22283;

XX

DT 29-JUL-1992 (first entry)

XX

DE Parathyroid hormone analogue N-terminus [1-34].

XX

KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;  
 KW disorders; psoriasis; cancer; burns.

XX  
 OS Homo sapiens.  
 XX  
 PN WO9204039-A.  
 XX  
 PD 19-MAR-1992.  
 XX  
 PF 30-AUG-1991; 91WO-US06218.  
 XX  
 PR 30-AUG-1990; 90US-0575219.  
 XX  
 PA (HOLI/) HOLICK M F.  
 XX  
 PI Holick MF;  
 XX  
 DR WPI; 1992-114063/14.  
 XX  
 PT Use of peptide having homology with parathyroid hormone - for  
 PT enhancement of cell proliferation for wound healing  
 XX  
 PS Disclosure; Fig 1; 34pp; English.  
 XX  
 CC The peptide can be easily synthesised by recombinant DNA or solid  
 CC phase peptide synthesis techniques. The peptide has > 50 percent  
 CC homology with the N-terminal 1-34 amino acids of human parathyroid  
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The  
 CC peptide may be used in a method for the treatment of hyperprolifer-  
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin  
 CC ulcerations by inhibition of cell proliferation and enhancement of  
 CC cell differentiation (agonist activity). They are also used to  
 CC enhance cell proliferation (antagonist activity) for wound healing.  
 CC They are also applicable in the promotion of new hair growth or  
 CC stimulation of the rate of hair growth e.g. following chemotherapy  
 CC or for treating alopecia e.g. male pattern baldness.  
 XX  
 SQ Sequence 34 AA;  
  
 Query Match 100.0%; Score 34; DB 13; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6  
 AAR41549  
 ID AAR41549 standard; protein; 34 AA.  
 XX  
 AC AAR41549;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 11-APR-1994 (first entry)  
 XX  
 DE [D-Ser3]hPTH (1-34)NH2.  
 XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;  
 KW hypoparathyroidism; hypertension.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 3  
 FT /note = "D-form residue"  
 FT Modified-site 34  
 FT /note = "C terminal is amidated"  
 XX  
 PN EP561412-A1.  
 XX  
 PD 22-SEP-1993.  
 XX  
 PF 18-MAR-1993; 93EP-0104500.  
 XX  
 PR 19-MAR-1992; 92JP-0063517.  
 PR 18-FEB-1993; 93JP-0029283.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Fukuda T, Nakagawa S, Taketomi S;  
 XX  
 DR WPI; 1993-296712/38.  
 XX  
 PT New parathyroid hormone derivs. - used for the treatment of  
 PT osteoporosis hypoparathyroidism and hypertension  
 XX  
 PS Example 1; Page 17; 37pp; English.  
 XX  
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;  
 CC AAR41549-R41582 - specific examples) show increased resistance to  
 CC proteases and a greater persistency of activity within the blood is  
 CC obtained. The proteins can be used to treat a number of bone and blood  
 CC disorders. This analogue was used as a test compound.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 14; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 7

AAR41570

ID AAR41570 standard; protein; 34 AA.

XX

AC AAR41570;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX  
 DE [Gln25]hPTH (1-34).  
 XX  
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;  
 KW hypoparathyroidism; hypertension.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP561412-A1.  
 XX  
 PD 22-SEP-1993.  
 XX  
 PF 18-MAR-1993; 93EP-0104500.  
 XX  
 PR 19-MAR-1992; 92JP-0063517.  
 PR 18-FEB-1993; 93JP-0029283.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Fukuda T, Nakagawa S, Taketomi S;  
 XX  
 DR WPI; 1993-296712/38.  
 XX  
 PT New parathyroid hormone derivs. - used for the treatment of  
 PT osteoporosis hypoparathyroidism and hypertension  
 XX  
 PS Example 1; Page 27; 37pp; English.  
 XX  
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;  
 CC AAR41549-R41582 - specific examples) show increased resistance to  
 CC proteases and a greater persistency of activity within the blood is  
 CC obtained. The proteins can be used to treat a number of bone and blood  
 CC disorders. This analogue was used as a test compound.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 14; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 8

AAR58291

ID AAR58291 standard; peptide; 34 AA.

XX

AC AAR58291;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;  
 KW hypoparathyroidism.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 26  
 FT /label= Other  
 FT /note= "Formyl-Lys."  
 FT Modified-site 27  
 FT /label= Other  
 FT /note= "Formyl-Lys."  
 FT Modified-site 34  
 FT /note= "in amide form"  
 XX  
 PN GB2269176-A.  
 XX  
 PD 02-FEB-1994.  
 XX  
 PF 12-JUL-1993; 93GB-0014384.  
 XX  
 PR 15-JUL-1992; 92GB-0015009.  
 PR 18-DEC-1992; 92GB-0026415.  
 PR 23-DEC-1992; 92GB-0026859.  
 PR 23-DEC-1992; 92GB-0026861.  
 PR 28-JAN-1993; 93GB-0001691.  
 PR 28-JAN-1993; 93GB-0001692.  
 PR 14-APR-1993; 93GB-0007673.  
 PR 19-APR-1993; 93GB-0008033.  
 XX  
 PA (SANO ) SANDOZ LTD.  
 PA (BAUE/) BAUER W.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;  
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;  
 PI Waelchli R, Rainer A;  
 XX  
 DR WPI; 1994-018352/03.  
 XX  
 PT New active para-thyroid hormone variants - used for treating or  
 PT preventing osteoporosis etc.  
 XX  
 PS Example 289; Page 47; 92pp; English.  
 XX  
 CC This peptide is an example of a highly generic formula covering  
 CC parathyroid hormone variants useful for treating or preventing bone  
 CC conditions associated with calcium depletion/resorption, in cases  
 CC where calcium fixation is required (esp. osteoporosis) or to treat  
 CC hypoparathyroidism.  
 XX  
 SQ Sequence 34 AA;  
  
 Query Match 100.0%; Score 34; DB 15; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

AC AAR58228;

XX

DT 20-SEP-1994 (first entry)

XX

DE [D-Asp30]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 30

FT /note= "D-form residue."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO ) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO ) SANDOZ PATENT GMBH.

PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

XX



PS Example 226; Page 45; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering  
CC parathyroid hormone variants useful for treating or preventing bone  
CC conditions associated with calcium depletion/resorption, in cases  
CC where calcium fixation is required (esp. osteoporosis) or to treat  
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 8.3e-27;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

#### RESULT 10

AAR58016

ID AAR58016 standard; peptide; 34 AA.

XX

AC AAR58016;

XX

DT 20-SEP-1994 (first entry)

XX

DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-alpha-isopropyl-Ser"

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO ) SANDOZ LTD.

PA (BAUE/) BAUER W.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;  
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;  
 PI Waelchli R, Rainer A;  
 XX  
 DR WPI; 1994-018352/03.  
 XX  
 PT New active para-thyroid hormone variants - used for treating or  
 PT preventing osteoporosis etc.  
 XX  
 PS Example 1; Page 30; 92pp; English.  
 XX  
 CC This peptide is an example of a highly generic formula covering  
 CC parathyroid hormone variants useful for treating or preventing bone  
 CC conditions associated with calcium depletion/resorption, in cases  
 CC where calcium fixation is required (esp. osteoporosis) or to treat  
 CC hypoparathyroidism.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 15; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 11  
 AAR58017  
 ID AAR58017 standard; peptide; 34 AA.  
 XX  
 AC AAR58017;  
 XX  
 DT 20-SEP-1994 (first entry)  
 XX  
 DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.  
 XX  
 KW Human parathyroid hormone; hPTH; variant; analogue;  
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;  
 KW hypoparathyroidism.  
 XX  
 OS Synthetic.  
 XX  

FH	Key	Location/Qualifiers
FT	Modified-site	26
FT		/note= "N-epsilon-Isopropyl-Lys"
FT	Modified-site	27
FT		/note= "N-epsilon-Isopropyl-Lys"
FT	Modified-site	34
FT		/note= "in amide form"

 XX  
 PN GB2269176-A.

XX  
 PD 02-FEB-1994.  
 XX  
 PF 12-JUL-1993; 93GB-0014384.  
 XX  
 PR 15-JUL-1992; 92GB-0015009.  
 PR 18-DEC-1992; 92GB-0026415.  
 PR 23-DEC-1992; 92GB-0026859.  
 PR 23-DEC-1992; 92GB-0026861.  
 PR 28-JAN-1993; 93GB-0001691.  
 PR 28-JAN-1993; 93GB-0001692.  
 PR 14-APR-1993; 93GB-0007673.  
 PR 19-APR-1993; 93GB-0008033.  
 XX  
 PA (SANO ) SANDOZ LTD.  
 PA (BAUE/) BAUER W.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;  
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;  
 PI Waelchli R, Rainer A;  
 XX  
 DR WPI; 1994-018352/03.  
 XX  
 PT New active para-thyroid hormone variants - used for treating or  
 PT preventing osteoporosis etc.  
 XX  
 PS Example 2; Page 32; 92pp; English.  
 XX  
 CC This peptide is an example of a highly generic formula covering  
 CC parathyroid hormone variants useful for treating or preventing bone  
 CC conditions associated with calcium depletion/resorption, in cases  
 CC where calcium fixation is required (esp. osteoporosis) or to treat  
 CC hypoparathyroidism.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 15; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 12

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX  
 KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;  
 KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;  
 KW eicosapentaenoic acid; EPA; antitumor.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9412530-A1.  
 XX  
 PD 09-JUN-1994.  
 XX  
 PF 29-NOV-1993; 93WO-HU00065.  
 XX  
 PR 30-NOV-1992; 92US-0984293.  
 XX  
 PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.  
 PA (SYNT-) SYNTHETIC PEPTIDES INC.  
 XX  
 PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;  
 PI Szederkenyi F, Vadasz Z;  
 XX  
 DR WPI; 1994-200194/24.  
 XX  
 PT New fatty acyl-peptide conjugates for inhibiting cell  
 PT proliferation - more active than free peptide, partic. for  
 PT treating tumours, virus-infected cells, psoriasis, etc.  
 XX  
 PS Disclosure; Fig. 1; 45pp; English.  
 XX  
 CC The peptides given in AAR55718-48 can each be conjugated through an  
 CC amide linkage with a polyunsaturated fatty acid moiety, such as  
 CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve  
 CC antiproliferative activity. The parathormone N-terminal fragment  
 CC inhibits osteoblast proliferation.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 15; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 13

AAR74521

ID AAR74521 standard; Peptide; 34 AA.

XX

AC AAR74521;

XX

DT 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX

DE Human parathyroid hormone (1-34).

XX  
 KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;  
 KW osteoporosis; hypercalcaemia; hyperparathroidism;  
 KW metabolic bone disease; human; veterinary medicine;  
 KW iontophoretic transdermal transport; recombinant E.coli.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9511988-A1.  
 XX  
 PD 04-MAY-1995.  
 XX  
 PF 25-OCT-1994; 94WO-US12205.  
 XX  
 PR 25-OCT-1993; 93US-0142551.  
 XX  
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
 XX  
 PI Oldenburg KR, Selick HE;  
 XX  
 DR WPI; 1995-178880/23.  
 XX  
 PT New active analogues of parathyroid hormone - with increased  
 PT activity, stability in serum etc., esp. for treating  
 PT osteoporosis, also related DNA and vectors  
 XX  
 PS Disclosure; Page 1; 109pp; English.  
 XX  
 CC This sequence represents residues 1-34 of human parathyroid hormone  
 CC (RPTH). This sequence was used in the production of analogues of the  
 CC truncated form of PTH. These analogues have increased activity and  
 CC longer serum half life than native PTH due to eg. substitution of Met  
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The  
 CC carboxy terminal may also be modified by the addition of a homoserine  
 CC residue or analogue, or by the addition of residues 35-84 of wild type  
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of  
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic  
 CC bone diseases in human or veterinary medicine. These peptides may also  
 CC have increased iontophoretic transdermal transport compared to wild type  
 CC PTH and can be produced in high yield in recombinant E.coli.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 16; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14  
 AAW99449  
 ID AAW99449 standard; peptide; 34 AA.  
 XX

AC AAW99449;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Human parathyroid hormone aal-34.  
 XX  
 KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;  
 KW spontaneous abortion; uterine contraction; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5880093-A.  
 XX  
 PD 09-MAR-1999.  
 XX  
 PF 05-APR-1995; 95US-0411726.  
 XX  
 PR 28-SEP-1992; 92IT-MI02331.  
 XX  
 PA (BAGN/) BAGNOLI F.  
 XX  
 PI Bagnoli F;  
 XX  
 DR WPI; 1996-162392/17.  
 XX  
 PT Use of composition containing parathormone or fragments - for  
 PT preventing premature birth or spontaneous abortion or for treating  
 PT unwanted uterine contractions  
 XX  
 PS Disclosure; Column 7-8; 11pp; English.  
 XX  
 CC Peptides AAW99448-W99452 represent all or part of the parathyroid  
 CC hormone (PTH; parathormone) sequence or related peptide. The peptides  
 CC are used for preventing premature birth, spontaneous abortion or unwanted  
 CC uterine contractions in a pregnant human patient.  
 CC (Note: this patent is the first Major Country Equivalent to Italian  
 CC Patent IT1255388).  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 17; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 15

AAR99978  
 ID AAR99978 standard; peptide; 34 AA.  
 XX  
 AC AAR99978;  
 XX  
 DT 30-APR-1997 (first entry)  
 XX

DE Human parathyroid hormone peptide fragment (1-34).  
 XX  
 KW cyclic parathyroid hormone fragment; calcium-regulating activity;  
 KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;  
 KW improved half life; calcium retention; bone.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19508672-A1.  
 XX  
 PD 12-SEP-1996.  
 XX  
 PF 10-MAR-1995; 95DE-1008672.  
 XX  
 PR 10-MAR-1995; 95DE-1008672.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;  
 XX  
 DR WPI; 1996-413519/42.  
 XX  
 PT Cyclic parathyroid hormone fragments with lactam bridge - have good  
 PT in vivo half life and are useful for treating osteoporosis and  
 PT preventing epidermal cell proliferation  
 XX  
 PS Disclosure; Page 9; 14pp; German.  
 XX  
 CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid  
 CC sequence of h, b, p, r or cPTH(1-34), opt. extended by up to 4 amino  
 CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at  
 CC the N-terminus, and are cyclised between positions 13 and 17. One of  
 CC these positions is occupied by L- or D- Orn or Lys, and the other by L-  
 CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for  
 CC treating osteoporosis and inhibit proliferation of epidermal cells (for  
 CC treating psoriasis). The CPTH have an improved half life in vivo than  
 CC known PTH fragments, increased mitogenicity and DNA-synthesising  
 CC capacity, reduced catabolic, calcium-mobilising activity and increased  
 CC activity for calcium retention and incorporation into bone. The  
 CC present sequence is that of human PTH peptide fragment (1-34).  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 17; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 16

AAR98951

ID AAR98951 standard; peptide; 34 AA.

XX

AC AAR98951;

XX  
 DT 15-JAN-1997 (first entry)  
 XX  
 DE Target peptide (PTH(1-34)) used in fusion protein construct.  
 XX  
 KW Fusion protein construct; isolation; purification;  
 KW growth hormone releasing factor; glucagon-like peptide 1;  
 KW parathyroid hormone; inclusion body; carbonic anhydrase.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9617942-A1.  
 XX  
 PD 13-JUN-1996.  
 XX  
 PF 07-DEC-1995; 95WO-US15800.  
 XX  
 PR 07-DEC-1994; 94US-0350530.  
 XX  
 PA (BION-) BIONEBRASKA INC.  
 XX  
 PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;  
 PI Partridge BE, Stout JS, Wagner FW;  
 XX  
 DR WPI; 1996-287186/29.  
 XX  
 PT Isolation and purificn of peptide(s) from fusion protein constructs  
 PT - which include a carbonic anhydrase and a variable fused  
 PT polypeptide  
 XX  
 PS Claim 18; Page 48; 67pp; English.  
 XX  
 CC A new method for the isolation and/or purification of a recombinant  
 CC peptide employs a fusion protein construct (FPC) comprising a  
 CC carbonic anhydrase and a variable fused polypeptide containing a  
 CC target peptide. The method comprises precipitating either the FPC or  
 CC a fragment of the FPC including the carbonic anhydrase. An  
 CC alternative method of producing the peptide comprises expressing the  
 CC FPC as part of an inclusion body. The target peptides of the FPC are  
 CC derived from growth hormone releasing factor (GRF), glucagon-like  
 CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence  
 CC corresponds to amino acids 1-34 of PTH.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 17; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

AAR98966

ID AAR98966 standard; Peptide; 34 AA.



XX  
 AC AAR98966;  
 XX  
 DT 02-DEC-1996 (first entry)  
 XX  
 DE PTH(1-34).  
 XX  
 KW PTH; parathyroid hormone; parathormone; C-amide;  
 KW C-amidated peptide; alpha-carboxamide; recombinant protein;  
 KW fusion protein; transpeptidation.  
 XX  
 OS Not specified.  
 XX  
 PN WO9617941-A2.  
 XX  
 PD 13-JUN-1996..  
 XX  
 PF 07-DEC-1995; 95WO-US15799.  
 XX  
 PR 07-DEC-1994; 94US-0350528.  
 XX  
 PA (BION-) BIONEBRASKA INC.  
 XX  
 PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;  
 PI Wagner FW;  
 XX  
 DR WPI; 1996-287185/29.  
 XX  
 PT Production of C-terminal alpha-carboxamidated peptide(s) - by  
 PT cleavage and transpeptidation of recombinant multicopy peptide(s) or  
 PT fusion constructs  
 XX  
 PS Claim 12; Page 70; 93pp; English.  
 XX  
 CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be  
 CC produced as C-terminal amidated peptides utilising novel recombinant  
 CC protein constructs (see also AAR98967-72) in which single or multiple  
 CC copies of the peptide are linked by intraconnecting peptides that  
 CC permit the construct to be selectively reacted to produce product  
 CC peptides having a C-terminal alpha-carboxamide. Expression cassettes  
 CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.  
 CC of the recombinant proteins in transformed E. coli host cells.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 17; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 18

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX  
 AC AAR88835;  
 XX  
 DT 07-OCT-1996 (first entry)  
 XX  
 DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH2.  
 XX  
 KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;  
 KW calcium regulation; reduced PKC activity; protein kinase C;  
 KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 10  
 FT /note= "forms peptide bond with Lys at posn. 26"  
 FT Modified-site 14  
 FT /note= "forms peptide bond with Asp at posn. 30"  
 FT Modified-site 26  
 FT /note= "forms peptide bond with Asn at posn. 10"  
 FT Modified-site 30  
 FT /note= "forms peptide bond with His at posn. 14"  
 FT Modified-site 34  
 FT /note= "amidated"  
 XX  
 PN CA2126299-A.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 20-JUN-1994; 94CA-2126299.  
 XX  
 PR 20-JUN-1994; 94CA-2126299.  
 XX  
 PA (WILL/) WILLICK G E.  
 XX  
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;  
 PI Willick GE;  
 XX  
 DR WPI; 1996-151754/16.  
 XX  
 PT New human parathyroid hormone analogues - which have increased  
 PT adenylyl cyclase activating activity, used for treating osteoporosis  
 XX  
 PS Claim 3; Fig 8; 2lpp; English.  
 XX  
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The  
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)  
 CC activity and reduce protein kinase C (PKC) activity. The analogues  
 CC can reverse the loss of bone and increase bone mass and density  
 CC without undesirable effects. They are useful for the treatment of  
 CC osteoporosis and other bone related disorders and disorders  
 CC involving bone cell calcium regulation.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 17; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
          |||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 19

AAW24273

ID AAW24273 standard; protein; 34 AA.

XX

AC AAW24273;

XX

DT 17-OCT-1997 (first entry)

XX

DE Wild type parathyroid hormone.

XX

KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;

KW electrotransportability; alpha-helix; beta-sheet.

XX

OS Homo sapiens.

XX

PN WO9639423-A2.

XX

PD 12-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09647.

XX

PR 06-JUN-1995; 95US-0468275.

XX

PA (ALZA ) ALZA CORP.

XX

PI Holladay LA, Oldenburg KR;

XX

DR WPI; 1997-043058/04.

XX

PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid

PT hormone and hirulog - which exhibit better or enhanced

PT electro-transportability through a body surface

XX

PS Claim 7; Fig 1A; 55pp; English.

XX

CC The sequences given in AAW24273-76 represent wildtype and analogues of  
CC parathyroid hormone (PTH). The analogues exhibit better/enhanced  
CC electrotransportability through a body surface, and are characterised  
CC by substituting one or more amino acid residues of the parent  
CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet  
CC segments of the parent polypeptide. An electrotransport device can  
CC deliver the polypeptide analogue through a body surface by electro-  
CC transport by including providing a therapeutically effective amount  
CC of the polypeptide analogue in a donor reservoir of the electrotransport  
CC device. The electrotransport flux of a polypeptide is increased by  
CC reducing the potential of the polypeptide for forming alpha-helix or  
CC beta-sheet segment.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 18; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

AAW19994

ID AAW19994 standard; peptide; 34 AA.

XX

AC AAW19994;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;

KW adenylate cyclase activity; bone growth; osteoporosis; fracture;

KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 34

FT /note= "amidated"

XX

PN WO9640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.

XX

PR 07-JUN-1995; 95US-0488105.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PI Chorev M, Rosenblatt M;

XX

DR WPI; 1997-051884/05.

XX

PT New cyclic analogues of parathyroid hormone - having di:sulphide or  
PT amide bond between residues 13 and 17 and/or between residues 26 and  
PT 30, useful for treating osteoporosis and bone fractures

XX

PS Claim 4; Page -; 23pp; English.

XX

CC AAW19994 is a cyclised peptide derived from the N-terminal sequence  
CC of human parathyroid hormone (PTH). The peptide is able to bind to  
CC PTH receptors and stimulate adenylate cyclase activity. Cyclised  
CC PTH peptides stimulate bone growth and thus are useful in the



PT 30, useful for treating osteoporosis and bone fractures  
 XX  
 PS Claim 6; Page -; 23pp; English.  
 XX  
 CC AAW20000 is a cyclised peptide derived from the N-terminal sequence  
 CC of human parathyroid hormone (PTH). The peptide is able to bind to  
 CC PTH receptors and stimulate adenylate cyclase activity. Cyclised  
 CC PTH peptides stimulate bone growth and thus are useful in the  
 CC treatment of osteoporosis and bone fractures. Optionally they may  
 CC be administered concurrently with antiresorptive therapy (e.g.  
 CC bisphosphonate and calcitonin).  
 CC N.B. sequence not given in the specification, created from known  
 CC sequence of amino acids 1-34 of human PTH.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 18; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 22

AAW20006

ID AAW20006 standard; peptide; 34 AA.

XX

AC AAW20006;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;  
 KW adenylate cyclase activity; bone growth; osteoporosis; fracture;  
 KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 26

FT /note= "joined via amide bond to residue 30"

FT Misc-difference 30

FT /note= "joined via amide bond to residue 26"

FT Misc-difference 34

FT /note= "amidated"

XX

PN WO9640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.  
 XX  
 PR 07-JUN-1995; 95US-0488105.  
 XX  
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
 XX  
 PI Chorev M, Rosenblatt M;  
 XX  
 DR WPI; 1997-051884/05.  
 XX  
 PT New cyclic analogues of parathyroid hormone - having di:sulphide or  
 PT amide bond between residues 13 and 17 and/or between residues 26 and  
 PT 30, useful for treating osteoporosis and bone fractures  
 XX  
 PS Claim 8; Page -; 23pp; English.  
 XX  
 CC AAW20006 is a cyclised peptide derived from the N-terminal sequence  
 CC of human parathyroid hormone (PTH). The peptide is able to bind to  
 CC PTH receptors and stimulate adenylate cyclase activity. Cyclised  
 CC PTH peptides stimulate bone growth and thus are useful in the  
 CC treatment of osteoporosis and bone fractures. Optionally they may  
 CC be administered concurrently with antiresorptive therapy (e.g.  
 CC bisphosphonate and calcitonin).  
 CC N.B. sequence not given in the specification, created from known  
 CC sequence of amino acids 1-34 of human PTH.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 18; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 23

AAW67291

ID AAW67291 standard; peptide; 34 AA.

XX

AC AAW67291;

XX

DT 22-DEC-1998 (first entry)

XX

DE Parathyroid hormone analogue #18.

XX

KW Parathyroid hormone; parathormone; bone growth; bone fracture;  
 KW osteoporosis; anti-resorptive therapy; calcitonin.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 12

FT /note= "1-amino-1-cyclohexanecarboxylic acid"

FT Modified-site 34

FT /note= "C-terminal amide"  
 XX  
 PN WO9830590-A2.  
 XX  
 PD 16-JUL-1998.  
 XX  
 PF 08-DEC-1997; 97WO-US22498.  
 XX  
 PR 07-MAR-1997; 97US-0813534.  
 PR 07-JAN-1997; 97US-0779768.  
 XX  
 PA (BIOM-) BIOMEASURE INC.  
 XX  
 PI Dong ZX;  
 XX  
 DR WPI; 1998-399065/34.  
 XX  
 PT Parathyroid hormone analogue peptide compounds - used for  
 PT stimulating bone growth, e.g. in treatment of bone fractures or  
 PT osteoporosis  
 XX  
 PS Claim 6; Page -; 24pp; English.  
 XX  
 CC The invention relates to peptides of formula (I) containing at least one  
 CC Acc (i.e. 1-amino-1-(3-9C cycloalkane)-carboxylic acid) residue.  
 CC (R1) (R2) A1-Val-A3-Glu-A5-Gln-A7-A8-His-Asn-A11-A12-Lys-His-A15-A-16-A17-  
 CC A-18-A19-Arg-A21-A22-A23-A24-Arg-Lys-A27-A28-A29-A30-A31-A32-A33-A34-R3  
 CC (I); where A1 = Ser, Ala or Dap; A3, A17 = Ser, Thr or Aib; A5, A7, A11,  
 CC A15 = Leu, Nle, Ile, Cha, beta -Nal, Trp, Pal, Acc, Phe or p-(X)-Phe; X  
 CC = OH, halo or Me; A8 = Met, Nva, Leu, Val, Ile, Cha, Acc or Nle; A12 =  
 CC Gly, Acc or Aib; A16 = Ser, Asn, Ala or Aib; A18 = Met, Nva, Leu, Val,  
 CC Ile, Nle, Acc, Cha or Aib; A19 = Glu or Aib; A21 = Val, Acc, Cha or Met;  
 CC A22 = Acc or Glu; A'23 = Trp, Acc or Cha; A24, A28 = Leu, Acc or Cha; A27  
 CC = Lys, Aib, Leu, hArg, Gln, Acc or Cha; A29 = Glu, Acc or Aib; A30 = Asp  
 CC or Lys; A31 = Val, Leu, Nle, Acc or Cha, or is deleted; A32 = His or is  
 CC deleted; A33 = Asn or is deleted; A34 = Phe, Tyr, Amp or Aib, or is  
 CC deleted; R1,R2 = H, 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl,  
 CC 11-20C naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C  
 CC hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; one of R1 and R2 may  
 CC also = COE; E = 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl, 11-20C  
 CC naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C  
 CC hydroxyphenylalkyl or 11-20C hydroxy-naphthylalkyl; R3 = OH, NH2, 1-12C  
 CC alkoxy or -NH-Y-CH2-Z; Y = 1-12C hydrocarbyl; Z = H, OH, COOH or CONH2.  
 CC The peptides are variants of fragments of parathyroid hormone (PTH) or  
 CC parathyroid hormone-related protein (PTHrP). They stimulate bone growth,  
 CC and are useful in the treatment of diseases or disorders associated with  
 CC bone growth deficiency, e.g. osteoporosis and bone fractures. They are  
 CC optionally used in conjunction with anti-resorptive therapy, e.g. with  
 CC bis-phosphonates or calcitonin. The present sequence represents a  
 CC specifically claimed peptide. NB: This sequence is not shown explicitly  
 CC in the patent but was generated using the sequence of human parathyroid  
 CC hormone as shown in Entrez Locus Number AAA29146.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 19; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;



Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 24

AAW61658

ID AAW61658 standard; peptide; 34 AA.

XX

AC AAW61658;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1998 (first entry)

XX

DE Parathyroid hormone analogue 1.

XX

KW parathyroid hormone; bone; osteoporosis; osteopenia.

XX

OS Homo sapiens.

XX

PN US5798225-A.

XX

PD 25-AUG-1998.

XX

PF 24-MAY-1995; 95US-0449500.

XX

PR 18-JAN-1994; 94US-0184328.

PR 14-JUL-1992; 92US-0915247.

PR 24-MAY-1995; 95US-0449500.

XX

PA (SYNT ) SYNTEX USA INC.

XX

PI Bach CT, Ho TH, Krstenansky JL, Nestor JJ, Vickery BH;

XX

DR WPI; 1998-480381/41.

XX

PT Recombinant production of modified parathyroid hormone or related  
PT peptide - having bone mass restoring activity which differs from  
PT naturally occurring PTH or PTHrP by changes comprising substitutions  
PT at one or more of positions 22-31

XX

PS Disclosure; Column 1/2; 65pp; English.

XX

CC The parathyroid hormone (PTH) analogues AAW61658-W61732 differ from  
CC naturally occurring PTH by changes comprising substitutions at on or  
CC more of positions 22-31. The bone mass restoring activity of the PTH  
CC analogues can be used to treat or prevent conditions characterised by  
CC a decrease in bone mass, e.g. osteoporosis or osteopenia.  
CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 19; Length 34;

Best Local Similarity 100.0%; Pred. No. 8.3e-27;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

AAW65975

ID AAW65975 standard; peptide; 34 AA.

XX

AC AAW65975;

XX

DT 25-MAR-2003 (updated)

DT 13-NOV-1998 (first entry)

XX

DE Human parathyroid hormone N-terminal fragment (residues 1-34).

XX

KW Parathyroid hormone; PTH; parathyroid hormone related peptide; PTHrp;

KW bone mass; trabecular bone; bone resorption; osteoporosis.

XX

OS Homo sapiens.

XX

PN US5807823-A.

XX

PD 15-SEP-1998.

XX

PF 24-MAY-1995; 95US-0449317.

XX

PR 18-JAN-1994; 94US-0184328.

PR 14-JUL-1992; 92US-0915247.

PR 24-MAY-1995; 95US-0449317.

XX

PA (SYNT ) SYNTEX USA INC.

XX

PI Krstenansky JL, Nestor JJ, Vickery BH;

XX

DR WPI; 1998-520168/44.

XX

PT Treatment of osteoporosis - by administration of modified

PT parathyroid hormone peptides

XX

PS Disclosure; Columns 1-2; 71pp; English.

XX

CC The invention relates to treatment of mammalian conditions characterised  
 CC by decreases in bone mass. The treatment comprises administering a  
 CC modified parathyroid hormone (PTH) or parathyroid hormone related peptide  
 CC (PTHrp) that differs from naturally occurring PTH or PTHrp by one or more  
 CC amino acid substitutions in positions 22-31. PTH and PTHrp are useful for  
 CC treatment of disorders characterised by decreasing bone mass, especially  
 CC osteoporosis. Use of PTH or PTHrp gives a sustainable increase in  
 CC trabecular bone by a different method to the prior art, which slowed down  
 CC bone resorption. The present sequence represents the N-terminal fragment  
 CC of human PTH (residues 1-34).

CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 19; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 26

AAAY50593

ID AAY50593 standard; peptide; 34 AA.

XX

AC      AAY50593;

XX

DT 09-FEB-2000 (first entry)

XX

DE     Resin bound cyclic peptide 26.

XX

KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;

KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;

KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;

KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.

XX

OS Synthetic.

XX

PN WO9952933-A1.

XX

PD 21-OCT-1999.

XX

PF 15-APR-1999; 99WO-US08435.

XX

PR 15-APR-1998; 98US-0081897.

XX

PA (RHON ) RHONE-POULENC RORER PHARM INC.

XX

PI Sledeski AW, Mencil JJ;

XX

DR WPI; 1999-633822/54.

XX

PT Convergent synthesis of peptides for treating e.g. bone disorders -

XX

PS Disclosure; Page 69; 85pp; English.

XX

CC This invention describes a novel method for the preparation of peptides

CC (II) that contain both cyclic and linear peptide fragments comprises

CC sequential reaction of a resin-bound linear fragment with the cyclic

CC fragment in N-protected form and optionally other linear fragments. The

CC products of the invention have osteopathic and hypotensive activity.

CC (II) bind to hPTH receptors and act as agonists or antagonists of hPTH.

CC The method is particularly used to prepare cyclic peptide analogs of

CC parathyroid hormone (PTH) or PTH-related peptides which are useful for

CC    treating diseases that respond to treatment with agents that bind to

CC receptors (with or without activation of adenylyl cyclase activity),

CC e.g. hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-

CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also  
CC for promoting repair of bone fractures. Separate synthesis of the cyclic



CC good storage stability, with a longer shelf life. A crystalline form of  
CC PTH is easily dissolved in a sterile solution for parenteral  
CC administration.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 20; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

#### RESULT 28

AAY14151

ID AAY14151 standard; protein; 34 AA.

XX

AC AAY14151;

XX

DT 26-JUL-1999 (first entry)

XX

DE Human parathyroid hormone PTH(1-34).

XX

KW Parathyroid hormone; human; PTH(1-34); PTH(1-84); osteoporosis; therapy;  
KW bone related disorder; hypoparathyroidism; pseudohypoparathyroidism;  
KW hypocalcaemic patient; diagnosis.

XX

OS Homo sapiens.

XX

PN EP920873-A2.

XX

PD 09-JUN-1999.

XX

PF 07-DEC-1998; 98EP-0123225.

XX

PR 09-DEC-1997; 97US-0069075.

XX

PA (ELIL ) LILLY & CO ELI.

XX

PI Chang C, Havel HA;

XX

DR WPI; 1999-315253/27.

XX

PT New parathyroid hormone solution useful for treating osteoporosis  
PT and related none disorders

XX

PS Claim 3; Page 8; 9pp; English.

XX

CC This sequence represents the human parathyroid hormone PTH(1-34).  
CC The invention relates to a parathyroid hormone solution comprising:  
CC parathyroid hormone, a stabilising agent, a buffering agent to maintain  
CC the pH of the solution between 3-7, and the balance being water.  
CC The composition is useful for treating osteoporosis and bone related  
CC disorders. The PTH composition is also useful for diagnosing  
CC hypoparathyroidism and pseudohypoparathyroidism in hypocalcaemic



Query Match 100.0%; Score 34; DB 20; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 30

AAW81871

ID AAW81871 standard; peptide; 34 AA.

XX

AC AAW81871;

XX

DT 05-FEB-1999 (first entry)

XX

DE Human PTH N-terminal peptide.

XX

KW PTH; parathyroid hormone; osteoporosis; treatment; osteopenia; PTHrP;

KW PTH-related peptide; analogue; bone mass.

XX

OS Homo sapiens.

XX

PN US5840837-A.

XX

PD 24-NOV-1998.

XX

PF 24-MAY-1995; 95US-0449447.

XX

PR 18-JAN-1994; 94US-0184328.

PR 14-JUL-1992; 92US-0915247.

PR 24-MAY-1995; 95US-0449447.

XX

PA (SYNT ) SYNTEX USA INC.

XX

PI Ho TH, Krstenansky JL, Nestor JJ;

XX

DR WPI; 1999-034119/03.

XX

PT Production of modified parathyroid hormone polypeptides by chemical  
PT synthesis - useful for restoring bone mass, in e.g. the treatment of  
PT osteoporosis and osteopenia

XX

PS Disclosure; Column 49-50; 60pp; English.

XX

CC AAW81871-W81952 are peptide fragments used in a method where synthetic  
CC polypeptide analogues of PTH (parathyroid hormone) or PTHrP (PTH-related  
CC peptide) and physiologically active truncated homologues and analogues  
CC of PTH and PTHrP are useful for the prophylaxis and treatment of  
CC osteopenia and osteoporosis and for restoring bone mass.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 20; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 31

ABJ10712

ID ABJ10712 standard; Peptide; 34 AA.

XX

AC ABJ10712;

XX

DT 02-DEC-2002 (first entry)

XX

DE Human parathyroid hormone analogue #8.

XX

KW Human; parathyroid hormone; parathyroid hormone-related protein;

KW PTH; PTHrP; analogue; abnormal CNS function; pancreatic function;

KW mineral metabolism; male infertility; abnormal blood pressure;

KW hypothalamic disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 8

FT /note= "D-form residue"

FT Modified-site 34

FT /note= "C-terminal amide"

XX

PN WO9957139-A2.

XX

PD 11-NOV-1999.

XX

PF 03-MAY-1999; 99WO-US09521.

XX

PR 05-MAY-1998; 98US-0072956.

XX

PA (SCRC ) SOC CONSEILS RECH & APPL SCI.

XX

PI Chorev M, Dong ZX, Rosenblatt M;

XX

DR WPI; 2000-038790/03.

XX

PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or

PT pancreatic functions, abnormal mineral metabolism and homeostasis, male

PT infertility, abnormal blood pressure or hypothalamic disease -

XX

PS Claim 11; Page 38; 49pp; English.

XX

CC The present invention provides a number of parathyroid hormone (PTH) or

CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2

CC receptor agonists or antagonists and can be used in the treatment of

CC disorders resulting from altered or excessive action of the PTH2

CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,

CC divergence from normal mineral metabolism and homeostasis, male



CC infertility, abnormal blood pressure or a hypothalamic disease. The  
CC present sequence is a peptide analogue of the invention.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 21; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 32

AAB07454

ID AAB07454 standard; peptide; 34 AA.

XX

AC AAB07454;

XX

DT 20-OCT-2000 (first entry)

XX

DE Amino acids 1-34 of the human parathyroid hormone.

XX

KW Parathyroid hormone; pTH; membrane adenylate cyclase; slimming product;  
KW thigh; hip; cellulite; skin strengthening.

XX

OS Homo sapiens.

XX

PN WO200040611-A1.

XX

PD 13-JUL-2000.

XX

PF 09-DEC-1999; 99WO-FR03110.

XX

PR 30-DEC-1998; 98FR-0016700.

XX

PA (SEDE-) SEDERMA.

XX

PI Lintner K;

XX

DR WPI; 2000-465954/40.

XX

PT New peptides from parathyroid hormone, useful as lipolytic agent in  
PT cosmetic or dermatological compositions, particularly for slimming -

XX

PS Disclosure; Page 1; 17pp; French.

XX

CC The present sequence represents the 1-34 amino acid region of  
CC human parathyroid hormone (pTH). Peptides derived from this region  
CC are used to modulate activity of membrane adenylate cyclase. The  
CC peptides are active when applied topically, and their activity  
CC may be increased by derivatisation with lipophilic groups. The  
CC peptides are used in cosmetic or dermatological compositions,  
CC especially as slimming products for application to thighs and hips,  
CC also for treating cellulite and for strengthening the skin.

XX

SQ Sequence 34 AA;

RESULT 33

ID AAY98017 standard; peptide; 34 AA.

AC      AAY98017;

DT 04-SEP-2000 (first entry)

DE Human amino-terminal modified parathyroid hormone analogue # 8.

KW Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;

KW bone disease; parathyroid hormone receptor; osteopaenia;

XX

XX

FT    Modified-site    1

XX

XX

XX

XX

XX

PA (TAKA/) TAKASU H.

XX

XX

XX

PT substitutions that confer PTH-1/PTH-2 receptor agonist properties,

Pl osteoporosis -

PS Disclosure; Page 64; 69pp; English.  
 xx

CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
CC cells, initiating signal transduction. It has been identified that the



PT useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain

XX

PS Example 5; Page 30; 88pp; Japanese.

XX

CC The present invention describes a human monoclonal antibody to  
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
CC its fragments, following the stimulation of PTHrP has the following  
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
CC the release of calcium from bone; or (c) inhibits elevation of blood  
CC calcium content. The monoclonal antibody can be used in the treatment  
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a  
CC human PTHrP peptide amino acid sequence from the present invention.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 21; Length 34;

Best Local Similarity 100.0%; Pred. No. 8.3e-27;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

#### RESULT 35

AAY68763

ID AAY68763 standard; peptide; 34 AA.

XX

AC AAY68763;

XX

DT 05-MAY-2000 (first entry)

XX

DE Amino acids 1-34 of a parathyroid hormone (pTH).

XX

KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;

KW slimming treatment; cellulite; skin firming.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "this residue is H-Ser"

FT Modified-site 34

FT /note= "this residue is Phe-OH"

XX

PN WO200004047-A1.

XX

PD 27-JAN-2000.

XX

PF 07-JUL-1999; 99WO-FR01687.

XX

PR 17-JUL-1998; 98FR-0009193.

XX  
PA (SEDE-) SEDERMA.  
XX  
PI Lintner K;  
XX  
DR WPI; 2000-171243/15.  
XX  
PT New parathyroid hormone fragment peptides, used as lipolysis stimulants  
PT in topically applied cosmetic compositions for slimming treatment of  
PT excessive weight in hips and thighs -  
XX  
PS Disclosure; Page 1; 18pp; French.  
XX  
CC The present sequence represents a parathyroid hormone (pTH) fragment,  
CC comprising amino acids 1-34. Parathyroid hormone fragments of the  
CC invention have lipolysis stimulating activity (especially when topically  
CC administered). The lipolytic activity of the peptides is enhanced when  
CC they are chemically modified to increase their lipophilicity. The  
CC peptides are used in cosmetic or dermatological compositions for skin  
CC care. They are especially used for slimming treatment of excessive  
CC weight in the thighs and hips, in the treatment of cellulite and for  
CC skin firming.  
XX  
SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 21; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 36

AAB84778

ID AAB84778 standard; Peptide; 34 AA.

XX

AC AAB84778;

XX

DT 25-JUL-2001 (first entry)

XX

DE Native rat parathyroid hormone peptide fragment #2.

XX

KW Osteopathic; calcium homeostasis regulator; parathyroid hormone; PTH;  
KW bone mass; osteoporosis.

XX

OS Rattus sp.

XX

PN WO200123521-A2.

XX

PD 05-APR-2001.

XX

PF 29-SEP-2000; 2000WO-US26818.

XX

PR 29-SEP-1999; 99US-0156927.

PR 25-FEB-2000; 2000US-0185060.

XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Juppner H;  
XX  
DR WPI; 2001-374252/39.  
XX  
PT New Parathyroid hormone (PTH) derivatives useful for treating  
PT conditions characterized by decreases in bone mass -  
XX  
PS Example 2; Page 67; 97pp; English.  
XX  
CC The present invention relates to parathyroid hormone (PTH) polypeptide  
CC derivatives, and the present sequence is one such derivative. PTH is a  
CC major regulator of calcium homeostasis. The PTH polypeptide derivatives  
CC are useful for treating conditions characterised by decreases in bone  
CC mass, such as old age osteoporosis and post-menopausal osteoporosis. The  
CC polypeptides are also useful for determining rates of bone reformation,  
CC bone resorption and/or bone remodeling, by administering the polypeptide  
CC to the patient and determining the uptake of the peptide into the bone,  
CC and effective bone mass-increasing amount to the peptide is administered  
CC by providing to the patient DNA encoding the peptide and expressing the  
CC peptide in vivo. The levels of cAMP and inositol phosphate can also be  
CC increased in a mammalian cell having PTH-1 receptors, by contacting the  
CC cell with a sufficient amount of the polypeptide.  
XX  
SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 22; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 37

AAB96898

ID AAB96898 standard; peptide; 34 AA.

XX

AC AAB96898;

XX

DT 13-JUL-2001 (first entry)

XX

DE Human parathyroid hormone(1-34).

XX

KW Rat; human; parathyroid hormone derivative; calcium homeostasis;  
KW hypercalcaemia; anaemia; bone disease; renal impairment; ulcer;  
KW myopathy; neuropathy; hyperparathyroidism; osteoporosis; fracture;  
KW cartilage disorder.

XX

OS Homo sapiens.

XX

PN WO200123427-A1.

XX

PD 05-APR-2001.

XX  
 PF 25-FEB-2000; 2000WO-US04716.  
 XX  
 PR 29-SEP-1999; 99US-0156927.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX  
 DR WPI; 2001-343161/36.  
 XX  
 PT Novel amino acid encoding polypeptides useful in the treatment of  
 PT osteoporosis -  
 XX  
 PS Example 2; Page 64; 100pp; English.  
 XX  
 CC The present invention provides a number of parathyroid hormone  
 CC derivatives based on the rat and human hormone sequences. These peptides  
 CC can be used in the treatment of human skeletal conditions, including  
 CC osteoporosis, fractures and cartilage disorders, disruption of calcium  
 CC homeostasis, which may cause severe bone disease, anaemia, renal  
 CC impairment, ulcers, myopathy and neuropathy, hypercalcaemia and  
 CC hyperparathyroidism. The present peptide was used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 38

AAB81079

ID AAB81079 standard; peptide; 34 AA.

XX

AC AAB81079;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human parathyroid hormone 1-34.

XX

KW Parathyroid hormone; PTH; blood calcium level regulator; osteopathic;  
 KW vulnerary; bone growth; bone healing; osteoporosis; fracture; human.

XX

OS Homo sapiens.

XX

PN WO200121643-A2.

XX

PD 29-MAR-2001.

XX

PF 21-SEP-2000; 2000WO-CA01083.

XX

PR 22-SEP-1999; 99US-0406813.  
 XX  
 PA (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 PI Barbier J, Morley P, Whitfield J, Willick GE;  
 XX  
 DR WPI; 2001-308081/32.  
 XX  
 PT New human parathyroid hormone (hPTH) analog useful for stimulating bone  
 PT growth, for restoring bone, for promotion of bone healing, and for  
 PT treating osteoporosis and normal fractures -  
 XX  
 PS Disclosure; Fig 1; 34pp; English.  
 XX  
 CC Parathyroid hormone (PTH) is a major regulator of blood calcium levels,  
 CC this invention relates to hPTH analogues, or their salts. Use of the  
 CC analogues results in osteopathic and vulnerary activity. The hPTH  
 CC analogues are useful for treating a warm-blooded animal for stimulating  
 CC bone growth, for restoring bone, and for the promotion of bone healing  
 CC during the treatment of osteoporosis and normal fractures. The present  
 CC sequence represents naturally occurring human parathyroid hormone.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 39

AAB91098

ID AAB91098 standard; Peptide; 34 AA.

XX

AC AAB91098;

XX

DT 22-JUN-2001 (first entry)

XX

DE Parathyroid hormone (PTH) related peptide SEQ ID NO:272.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US13576.

XX

PR 17-MAY-1999; 99US-0134406.



PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX  
 PA (CONJ-) CONJUCHEM INC.  
 XX  
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX  
 DR WPI; 2001-112059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT -  
 XX  
 PS Disclosure; Page 281; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

#### RESULT 40

ABJ05328

ID ABJ05328 standard; Peptide; 34 AA.

XX

AC ABJ05328;

XX

DT 08-NOV-2002 (first entry)

XX

DE Human PTH(1-34) peptide.

XX

KW Target peptide production; fusion peptide; protease-susceptible linker;  
 KW parathyroid hormone; PTH; high expression rate;  
 KW pharmaceutical application.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200236762-A1.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 29-OCT-2001; 2001WO-JP09476.  
 XX  
 PR 30-OCT-2000; 2000JP-0331170.  
 PR 27-JUN-2001; 2001JP-0195522.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Yamada T, Suenaga M;  
 XX  
 DR WPI; 2002-417275/44.  
 DR N-PSDB; ABT06798.  
 XX  
 PT Production of target peptide comprises cleavage of fusion peptide with  
 PT parathyroid hormone peptide for efficient manufacture of target peptide  
 PT without the need to remove N-terminal methionine -  
 XX  
 PS Disclosure; Page 14; 103pp; Japanese.  
 XX  
 CC The invention comprises a method of producing a target peptide. The  
 CC C-terminal end of the target peptide is fused via a protease-susceptible  
 CC linker to parathyroid hormone (PTH) residues 1-34. The method of the  
 CC invention is useful for the clean and efficient production of a target  
 CC peptide at a high expression rate on an industrial scale without the need  
 CC to remove the N-terminal methionine from the product. The peptides  
 CC produced by the method of the invention are suitable for pharmaceutical  
 CC and other uses. The present peptide sequence was used in the invention.  
 XX  
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 23; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-27;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:34:18  
 Job time : 36.5171 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 11.5452 Seconds  
(without alignments)  
124.604 Million cell updates/sec

Title: US-09-843-221A-161  
Perfect score: 34  
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28  
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	34	100.0	34	1	US-07-765-373-1
2	34	100.0	34	1	US-08-033-099-1
3	34	100.0	34	1	US-08-262-495C-1
4	34	100.0	34	1	US-07-915-247A-1
5	34	100.0	34	1	US-08-443-863-1
6	34	100.0	34	1	US-08-448-070-1
7	34	100.0	34	1	US-08-488-105-7
8	34	100.0	34	1	US-08-468-275-6
9	34	100.0	34	1	US-08-449-500-1
10	34	100.0	34	1	US-08-449-317A-1
11	34	100.0	34	2	US-08-142-551B-2

12	34	100.0	34	2	US-08-477-022-1	Sequence 1, Appli
13	34	100.0	34	2	US-08-449-447-1	Sequence 1, Appli
14	34	100.0	34	2	US-08-835-231-13	Sequence 13, Appl
15	34	100.0	34	2	US-08-184-328-1	Sequence 1, Appli
16	34	100.0	34	2	US-08-411-726-2	Sequence 2, Appli
17	34	100.0	34	2	US-08-691-647C-5	Sequence 5, Appli
18	34	100.0	34	2	US-08-521-097-1	Sequence 1, Appli
19	34	100.0	34	3	US-09-044-536A-1	Sequence 1, Appli
20	34	100.0	34	3	US-08-904-760B-22	Sequence 22, Appl
21	34	100.0	34	3	US-09-108-661-13	Sequence 13, Appl
22	34	100.0	34	4	US-09-007-466-6	Sequence 6, Appli
23	34	100.0	34	4	US-09-406-813-1	Sequence 1, Appli
24	34	100.0	34	4	US-08-952-980B-6	Sequence 6, Appli
25	34	100.0	34	4	US-09-228-990-1	Sequence 1, Appli
26	34	100.0	34	4	US-09-447-800-8	Sequence 8, Appli
27	34	100.0	34	4	US-09-536-785A-22	Sequence 22, Appl
28	34	100.0	34	4	US-09-442-989-26	Sequence 26, Appl
29	34	100.0	34	5	PCT-US95-15800-22	Sequence 22, Appl
30	34	100.0	35	1	US-08-256-363-3	Sequence 3, Appli
31	34	100.0	36	1	US-08-256-363-4	Sequence 4, Appli
32	34	100.0	37	1	US-08-440-117-1	Sequence 1, Appli
33	34	100.0	37	3	US-09-068-738A-16	Sequence 16, Appl
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35	34	100.0	38	1	US-08-232-849-1	Sequence 1, Appli
36	34	100.0	38	2	US-08-625-586-1	Sequence 1, Appli
37	34	100.0	38	3	US-09-128-401-1	Sequence 1, Appli
38	33	97.1	33	4	US-09-447-800-9	Sequence 9, Appli
39	33	97.1	34	3	US-08-903-497A-1	Sequence 1, Appli
40	33	97.1	34	4	US-09-635-076-1	Sequence 1, Appli
41	33	97.1	34	4	US-09-447-800-1	Sequence 1, Appli
42	33	97.1	34	4	US-09-447-800-2	Sequence 2, Appli
43	33	97.1	34	4	US-09-447-800-5	Sequence 5, Appli
44	33	97.1	36	1	US-08-112-024-2	Sequence 2, Appli
45	32	94.1	33	1	US-08-256-363-1	Sequence 1, Appli
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50	31	91.2	31	2	US-08-691-647C-1	Sequence 1, Appli
51	31	91.2	31	2	US-08-691-647C-6	Sequence 6, Appli
52	31	91.2	31	3	US-08-904-760B-1	Sequence 1, Appli
53	31	91.2	31	3	US-08-904-760B-6	Sequence 6, Appli
54	31	91.2	31	3	US-08-904-760B-14	Sequence 14, Appl
55	31	91.2	31	3	US-08-904-760B-32	Sequence 32, Appl
56	31	91.2	31	4	US-09-406-813-2	Sequence 2, Appli
57	31	91.2	31	4	US-09-536-785A-1	Sequence 1, Appli
58	31	91.2	31	4	US-09-536-785A-6	Sequence 6, Appli
59	31	91.2	31	4	US-09-536-785A-14	Sequence 14, Appl
60	31	91.2	31	4	US-09-536-785A-32	Sequence 32, Appl
61	30	88.2	30	1	US-08-262-495C-5	Sequence 5, Appli
62	29	85.3	34	4	US-09-449-632-24	Sequence 24, Appl
63	28	82.4	28	4	US-09-448-867-12	Sequence 12, Appl
64	28	82.4	38	5	PCT-US95-15800-29	Sequence 29, Appl
65	27	79.4	28	4	US-09-448-867-8	Sequence 8, Appli
66	27	79.4	28	4	US-09-448-867-10	Sequence 10, Appl
67	26	76.5	28	4	US-09-406-813-3	Sequence 3, Appli
68	26	76.5	29	4	US-09-406-813-4	Sequence 4, Appli

69	26	76.5	30	1	US-08-262-495C-6	Sequence 6, Appli
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88	26	76.5	31	4	US-09-536-785A-4	Sequence 4, Appli
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90	26	76.5	31	4	US-09-536-785A-8	Sequence 8, Appli
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93	26	76.5	31	4	US-09-536-785A-15	Sequence 15, Appl
94	26	76.5	31	4	US-09-536-785A-16	Sequence 16, Appl
95	26	76.5	31	4	US-09-536-785A-17	Sequence 17, Appl
96	26	76.5	34	1	US-08-262-495C-2	Sequence 2, Appli
97	26	76.5	34	3	US-08-904-760B-9	Sequence 9, Appli
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102	25	73.5	31	4	US-09-536-785A-21	Sequence 21, Appl
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111	23	67.6	34	3	US-09-044-536A-11	Sequence 11, Appl
112	23	67.6	34	3	US-09-044-536A-12	Sequence 12, Appl
113	21	61.8	31	3	US-08-904-760B-18	Sequence 18, Appl
114	21	61.8	31	3	US-08-904-760B-19	Sequence 19, Appl
115	21	61.8	31	3	US-08-904-760B-20	Sequence 20, Appl
116	21	61.8	31	4	US-09-536-785A-18	Sequence 18, Appl
117	21	61.8	31	4	US-09-536-785A-19	Sequence 19, Appl
118	21	61.8	31	4	US-09-536-785A-20	Sequence 20, Appl
119	21	61.8	34	3	US-09-044-536A-26	Sequence 26, Appl
120	20	58.8	34	3	US-09-044-536A-25	Sequence 25, Appl
121	20	58.8	34	4	US-08-952-980B-9	Sequence 9, Appli
122	19	55.9	34	3	US-08-903-497A-3	Sequence 3, Appli
123	19	55.9	34	4	US-09-635-076-3	Sequence 3, Appli
124	18	52.9	28	4	US-09-448-867-6	Sequence 6, Appli
125	18	52.9	34	1	US-07-915-247A-2	Sequence 2, Appli

126	18	52.9	34	1	US-08-443-863-2	Sequence 2, Appli
127	18	52.9	34	1	US-08-448-070-2	Sequence 2, Appli
128	18	52.9	34	1	US-08-488-105-2	Sequence 2, Appli
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130	18	52.9	34	1	US-08-449-500-2	Sequence 2, Appli
131	18	52.9	34	1	US-08-449-317A-2	Sequence 2, Appli
132	18	52.9	34	2	US-08-477-022-2	Sequence 2, Appli
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134	18	52.9	34	2	US-08-184-328-2	Sequence 2, Appli
135	18	52.9	34	2	US-08-521-097-2	Sequence 2, Appli
136	18	52.9	34	3	US-09-044-536A-18	Sequence 18, Appl
137	18	52.9	34	3	US-09-044-536A-19	Sequence 19, Appl
138	17	50.0	28	4	US-09-448-867-1	Sequence 1, Appli
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140	17	50.0	28	4	US-09-448-867-4	Sequence 4, Appli
141	17	50.0	34	1	US-08-488-105-1	Sequence 1, Appli
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152	16	47.1	34	1	US-08-449-317A-3	Sequence 3, Appli
153	16	47.1	34	2	US-08-477-022-3	Sequence 3, Appli
154	16	47.1	34	2	US-08-449-447-3	Sequence 3, Appli
155	16	47.1	34	2	US-08-184-328-3	Sequence 3, Appli
156	16	47.1	34	2	US-08-521-097-3	Sequence 3, Appli
157	15	44.1	34	1	US-08-488-105-4	Sequence 4, Appli
158	15	44.1	34	1	US-08-488-105-6	Sequence 6, Appli
159	15	44.1	34	1	US-08-488-105-10	Sequence 10, Appl
160	15	44.1	34	1	US-08-488-105-11	Sequence 11, Appl
161	15	44.1	34	1	US-08-488-105-16	Sequence 16, Appl
162	15	44.1	34	1	US-08-488-105-18	Sequence 18, Appl
163	15	44.1	34	1	US-08-449-500-79	Sequence 79, Appl
164	15	44.1	34	1	US-08-449-317A-79	Sequence 79, Appl
165	15	44.1	34	2	US-08-142-551B-3	Sequence 3, Appli
166	15	44.1	34	2	US-08-477-022-79	Sequence 79, Appl
167	15	44.1	34	2	US-08-449-447-79	Sequence 79, Appl
168	15	44.1	34	2	US-08-184-328-79	Sequence 79, Appl
169	15	44.1	34	2	US-08-521-097-79	Sequence 79, Appl
170	15	44.1	34	3	US-09-044-536A-27	Sequence 27, Appl
171	15	44.1	34	3	US-09-044-536A-29	Sequence 29, Appl
172	15	44.1	34	3	US-08-903-497A-4	Sequence 4, Appli
173	15	44.1	34	4	US-09-635-076-4	Sequence 4, Appli
174	15	44.1	35	2	US-08-142-551B-4	Sequence 4, Appli
175	15	44.1	35	2	US-08-142-551B-5	Sequence 5, Appli
176	15	44.1	35	2	US-08-142-551B-7	Sequence 7, Appli
177	15	44.1	35	2	US-08-142-551B-11	Sequence 11, Appl
178	15	44.1	35	2	US-08-142-551B-12	Sequence 12, Appl
179	15	44.1	35	2	US-08-142-551B-13	Sequence 13, Appl
180	15	44.1	35	2	US-08-142-551B-14	Sequence 14, Appl
181	15	44.1	35	2	US-08-142-551B-15	Sequence 15, Appl
182	15	44.1	35	2	US-08-142-551B-16	Sequence 16, Appl

183	15	44.1	35	2	US-08-142-551B-17	Sequence 17, Appl
184	15	44.1	35	2	US-08-142-551B-18	Sequence 18, Appl
185	15	44.1	35	2	US-08-142-551B-19	Sequence 19, Appl
186	15	44.1	35	2	US-08-142-551B-20	Sequence 20, Appl
187	15	44.1	35	2	US-08-142-551B-21	Sequence 21, Appl
188	15	44.1	35	2	US-08-142-551B-22	Sequence 22, Appl
189	15	44.1	35	2	US-08-142-551B-23	Sequence 23, Appl
190	15	44.1	35	2	US-08-142-551B-24	Sequence 24, Appl
191	15	44.1	35	2	US-08-142-551B-25	Sequence 25, Appl
192	15	44.1	35	2	US-08-142-551B-26	Sequence 26, Appl
193	15	44.1	35	2	US-08-142-551B-27	Sequence 27, Appl
194	15	44.1	35	2	US-08-142-551B-28	Sequence 28, Appl
195	15	44.1	35	2	US-08-142-551B-29	Sequence 29, Appl
196	15	44.1	35	2	US-08-142-551B-30	Sequence 30, Appl
197	15	44.1	35	2	US-08-142-551B-31	Sequence 31, Appl
198	15	44.1	35	2	US-08-142-551B-32	Sequence 32, Appl
199	15	44.1	35	2	US-08-142-551B-33	Sequence 33, Appl
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201	15	44.1	35	2	US-08-142-551B-35	Sequence 35, Appl
202	15	44.1	35	2	US-08-142-551B-36	Sequence 36, Appl
203	15	44.1	35	2	US-08-142-551B-37	Sequence 37, Appl
204	15	44.1	35	2	US-08-142-551B-38	Sequence 38, Appl
205	15	44.1	35	2	US-08-142-551B-39	Sequence 39, Appl
206	15	44.1	35	2	US-08-142-551B-40	Sequence 40, Appl
207	15	44.1	35	2	US-08-142-551B-41	Sequence 41, Appl
208	15	44.1	35	2	US-08-142-551B-42	Sequence 42, Appl
209	15	44.1	35	2	US-08-142-551B-43	Sequence 43, Appl
210	15	44.1	35	2	US-08-142-551B-44	Sequence 44, Appl
211	15	44.1	35	2	US-08-142-551B-45	Sequence 45, Appl
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214	15	44.1	35	2	US-08-142-551B-48	Sequence 48, Appl
215	15	44.1	35	2	US-08-142-551B-49	Sequence 49, Appl
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219	15	44.1	35	2	US-08-142-551B-53	Sequence 53, Appl
220	15	44.1	35	2	US-08-142-551B-54	Sequence 54, Appl
221	15	44.1	35	2	US-08-142-551B-55	Sequence 55, Appl
222	15	44.1	35	2	US-08-142-551B-56	Sequence 56, Appl
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229	15	44.1	35	2	US-08-142-551B-63	Sequence 63, Appl
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231	15	44.1	35	2	US-08-142-551B-65	Sequence 65, Appl
232	15	44.1	35	2	US-08-142-551B-66	Sequence 66, Appl
233	15	44.1	35	2	US-08-142-551B-67	Sequence 67, Appl
234	15	44.1	35	2	US-08-142-551B-68	Sequence 68, Appl
235	15	44.1	35	2	US-08-142-551B-70	Sequence 70, Appl
236	15	44.1	35	2	US-08-142-551B-73	Sequence 73, Appl
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239	15	44.1	35	2	US-08-142-551B-94	Sequence 94, Appl

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241	14	41.2	34	1	US-08-488-105-9	Sequence 9, Appli
242	14	41.2	34	1	US-08-488-105-15	Sequence 15, Appl
243	14	41.2	34	3	US-08-903-497A-7	Sequence 7, Appli
244	14	41.2	34	4	US-09-635-076-7	Sequence 7, Appli
245	14	41.2	35	2	US-08-142-551B-69	Sequence 69, Appl
246	14	41.2	35	2	US-08-142-551B-71	Sequence 71, Appl
247	14	41.2	35	2	US-08-142-551B-115	Sequence 115, App
248	14	41.2	35	2	US-08-142-551B-116	Sequence 116, App
249	14	41.2	35	2	US-08-142-551B-117	Sequence 117, App
250	14	41.2	35	2	US-08-142-551B-118	Sequence 118, App
251	13	38.2	30	3	US-08-904-760B-33	Sequence 33, Appl
252	13	38.2	30	3	US-08-904-760B-34	Sequence 34, Appl
253	13	38.2	30	3	US-08-904-760B-35	Sequence 35, Appl
254	13	38.2	30	4	US-09-536-785A-33	Sequence 33, Appl
255	13	38.2	30	4	US-09-536-785A-34	Sequence 34, Appl
256	13	38.2	30	4	US-09-536-785A-35	Sequence 35, Appl
257	13	38.2	34	3	US-09-044-536A-28	Sequence 28, Appl
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264	13	38.2	35	2	US-08-142-551B-114	Sequence 114, App
265	12	35.3	34	1	US-08-049-402-2	Sequence 2, Appli
266	12	35.3	34	1	US-08-526-987-2	Sequence 2, Appli
267	12	35.3	34	3	US-08-903-497A-5	Sequence 5, Appli
268	12	35.3	34	4	US-09-635-076-5	Sequence 5, Appli
269	12	35.3	35	2	US-08-142-551B-76	Sequence 76, Appl
270	12	35.3	35	2	US-08-142-551B-77	Sequence 77, Appl
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275	12	35.3	35	2	US-08-142-551B-110	Sequence 110, App
276	11	32.4	34	1	US-08-488-105-5	Sequence 5, Appli
277	11	32.4	34	1	US-08-488-105-12	Sequence 12, Appl
278	11	32.4	34	1	US-08-488-105-17	Sequence 17, Appl
279	11	32.4	34	1	US-08-449-500-61	Sequence 61, Appl
280	11	32.4	34	1	US-08-449-317A-61	Sequence 61, Appl
281	11	32.4	34	2	US-08-477-022-61	Sequence 61, Appl
282	11	32.4	34	2	US-08-449-447-61	Sequence 61, Appl
283	11	32.4	34	2	US-08-184-328-61	Sequence 61, Appl
284	11	32.4	34	2	US-08-521-097-61	Sequence 61, Appl
285	11	32.4	34	4	US-09-449-632-22	Sequence 22, Appl
286	11	32.4	35	2	US-08-142-551B-79	Sequence 79, Appl
287	11	32.4	35	2	US-08-142-551B-81	Sequence 81, Appl
288	11	32.4	35	2	US-08-142-551B-104	Sequence 104, App
289	11	32.4	35	2	US-08-142-551B-105	Sequence 105, App
290	11	32.4	35	2	US-08-142-551B-106	Sequence 106, App
291	11	32.4	35	2	US-08-142-551B-121	Sequence 121, App
292	11	32.4	35	2	US-08-142-551B-122	Sequence 122, App
293	11	32.4	35	2	US-08-142-551B-123	Sequence 123, App
294	10	29.4	34	1	US-08-033-099-2	Sequence 2, Appli
295	10	29.4	34	3	US-09-044-536A-20	Sequence 20, Appl
296	10	29.4	34	3	US-09-044-536A-21	Sequence 21, Appl



297	10	29.4	34	3	US-09-044-536A-22	Sequence 22, Appl
298	10	29.4	34	3	US-09-044-536A-24	Sequence 24, Appl
299	10	29.4	34	3	US-08-903-497A-6	Sequence 6, Appli
300	10	29.4	34	4	US-09-635-076-6	Sequence 6, Appli
301	10	29.4	35	2	US-08-142-551B-82	Sequence 82, Appl
302	10	29.4	35	2	US-08-142-551B-83	Sequence 83, Appl
303	10	29.4	35	2	US-08-142-551B-84	Sequence 84, Appl
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305	10	29.4	35	2	US-08-142-551B-102	Sequence 102, App
306	10	29.4	35	2	US-08-142-551B-103	Sequence 103, App
307	10	29.4	35	2	US-08-142-551B-120	Sequence 120, App
308	9	26.5	28	4	US-09-228-990-54	Sequence 54, Appl
309	9	26.5	28	4	US-09-228-990-62	Sequence 62, Appl
310	9	26.5	28	4	US-09-228-990-65	Sequence 65, Appl
311	9	26.5	28	4	US-09-228-990-79	Sequence 79, Appl
312	9	26.5	28	4	US-09-442-989-22	Sequence 22, Appl
313	9	26.5	28	4	US-09-442-989-25	Sequence 25, Appl
314	9	26.5	29	4	US-09-406-813-8	Sequence 8, Appli
315	9	26.5	29	4	US-09-228-990-53	Sequence 53, Appl
316	9	26.5	29	4	US-09-228-990-63	Sequence 63, Appl
317	9	26.5	30	4	US-09-228-990-52	Sequence 52, Appl
318	9	26.5	30	4	US-09-228-990-64	Sequence 64, Appl
319	9	26.5	31	3	US-08-904-760B-13	Sequence 13, Appl
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321	9	26.5	31	4	US-09-228-990-4	Sequence 4, Appli
322	9	26.5	31	4	US-09-228-990-5	Sequence 5, Appli
323	9	26.5	31	4	US-09-228-990-6	Sequence 6, Appli
324	9	26.5	31	4	US-09-228-990-7	Sequence 7, Appli
325	9	26.5	31	4	US-09-228-990-8	Sequence 8, Appli
326	9	26.5	31	4	US-09-228-990-9	Sequence 9, Appli
327	9	26.5	31	4	US-09-228-990-10	Sequence 10, Appl
328	9	26.5	31	4	US-09-228-990-20	Sequence 20, Appl
329	9	26.5	31	4	US-09-228-990-21	Sequence 21, Appl
330	9	26.5	31	4	US-09-228-990-22	Sequence 22, Appl
331	9	26.5	31	4	US-09-228-990-23	Sequence 23, Appl
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334	9	26.5	31	4	US-09-228-990-26	Sequence 26, Appl
335	9	26.5	31	4	US-09-228-990-27	Sequence 27, Appl
336	9	26.5	31	4	US-09-228-990-36	Sequence 36, Appl
337	9	26.5	31	4	US-09-228-990-37	Sequence 37, Appl
338	9	26.5	31	4	US-09-228-990-38	Sequence 38, Appl
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341	9	26.5	31	4	US-09-228-990-48	Sequence 48, Appl
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344	9	26.5	31	4	US-09-228-990-51	Sequence 51, Appl
345	9	26.5	31	4	US-09-228-990-69	Sequence 69, Appl
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347	9	26.5	31	4	US-09-228-990-74	Sequence 74, Appl
348	9	26.5	31	4	US-09-228-990-81	Sequence 81, Appl
349	9	26.5	31	4	US-09-228-990-82	Sequence 82, Appl
350	9	26.5	31	4	US-09-228-990-83	Sequence 83, Appl
351	9	26.5	31	4	US-09-228-990-84	Sequence 84, Appl
352	9	26.5	31	4	US-09-228-990-85	Sequence 85, Appl
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360	9	26.5	31	4	US-09-442-989-7	Sequence 7, Appli
361	9	26.5	31	4	US-09-442-989-8	Sequence 8, Appli
362	9	26.5	31	4	US-09-442-989-17	Sequence 17, Appl
363	9	26.5	31	4	US-09-442-989-32	Sequence 32, Appl
364	9	26.5	34	3	US-09-044-536A-2	Sequence 2, Appli
365	9	26.5	34	3	US-09-044-536A-23	Sequence 23, Appl
366	9	26.5	34	4	US-09-228-990-46	Sequence 46, Appl
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369	9	26.5	35	2	US-08-142-551B-85	Sequence 85, Appl
370	9	26.5	35	2	US-08-142-551B-86	Sequence 86, Appl
371	9	26.5	35	2	US-08-142-551B-87	Sequence 87, Appl
372	9	26.5	35	2	US-08-142-551B-88	Sequence 88, Appl
373	9	26.5	35	2	US-08-142-551B-89	Sequence 89, Appl
374	9	26.5	35	2	US-08-142-551B-91	Sequence 91, Appl
375	9	26.5	35	2	US-08-142-551B-92	Sequence 92, Appl
376	9	26.5	35	2	US-08-142-551B-93	Sequence 93, Appl
377	9	26.5	35	2	US-08-142-551B-95	Sequence 95, Appl
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379	9	26.5	35	2	US-08-142-551B-97	Sequence 97, Appl
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383	9	26.5	35	3	US-09-044-536A-30	Sequence 30, Appl
384	9	26.5	36	3	US-09-044-536A-31	Sequence 31, Appl
385	9	26.5	37	3	US-09-044-536A-32	Sequence 32, Appl
386	9	26.5	38	3	US-09-044-536A-33	Sequence 33, Appl
387	9	26.5	39	3	US-09-044-536A-34	Sequence 34, Appl
388	9	26.5	40	3	US-09-044-536A-35	Sequence 35, Appl
389	8	23.5	28	4	US-09-228-990-78	Sequence 78, Appl
390	8	23.5	28	4	US-09-442-989-24	Sequence 24, Appl
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393	8	23.5	31	1	US-07-778-926-14	Sequence 14, Appl
394	8	23.5	31	4	US-09-228-990-11	Sequence 11, Appl
395	8	23.5	31	4	US-09-228-990-19	Sequence 19, Appl
396	8	23.5	31	4	US-09-228-990-28	Sequence 28, Appl
397	8	23.5	31	4	US-09-228-990-35	Sequence 35, Appl
398	8	23.5	31	4	US-09-228-990-40	Sequence 40, Appl
399	8	23.5	31	4	US-09-228-990-45	Sequence 45, Appl
400	8	23.5	31	4	US-09-228-990-66	Sequence 66, Appl
401	8	23.5	31	4	US-09-228-990-67	Sequence 67, Appl
402	8	23.5	31	4	US-09-228-990-68	Sequence 68, Appl
403	8	23.5	31	4	US-09-228-990-73	Sequence 73, Appl
404	8	23.5	31	4	US-09-228-990-76	Sequence 76, Appl
405	8	23.5	31	4	US-09-228-990-80	Sequence 80, Appl
406	8	23.5	31	4	US-09-442-989-16	Sequence 16, Appl
407	8	23.5	32	1	US-07-778-926-18	Sequence 18, Appl
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409	8	23.5	34	1	US-07-778-926-11	Sequence 11, Appl
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413	8	23.5	34	4	US-09-442-989-19	Sequence 19, Appl
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415	8	23.5	36	1	US-07-778-926-19	Sequence 19, Appl
416	8	23.5	37	1	US-07-778-926-8	Sequence 8, Appli
417	8	23.5	38	1	US-07-778-926-12	Sequence 12, Appl
418	8	23.5	39	1	US-07-778-926-16	Sequence 16, Appl
419	8	23.5	40	1	US-07-778-926-20	Sequence 20, Appl
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421	7	20.6	31	4	US-09-406-813-9	Sequence 9, Appli
422	7	20.6	31	4	US-09-228-990-12	Sequence 12, Appl
423	7	20.6	31	4	US-09-228-990-18	Sequence 18, Appl
424	7	20.6	31	4	US-09-228-990-29	Sequence 29, Appl
425	7	20.6	31	4	US-09-228-990-34	Sequence 34, Appl
426	7	20.6	31	4	US-09-228-990-41	Sequence 41, Appl
427	7	20.6	31	4	US-09-228-990-44	Sequence 44, Appl
428	7	20.6	31	4	US-09-442-989-9	Sequence 9, Appli
429	7	20.6	31	4	US-09-442-989-15	Sequence 15, Appl
430	7	20.6	32	1	US-07-778-926-3	Sequence 3, Appli
431	7	20.6	32	1	US-08-305-799A-1	Sequence 1, Appli
432	7	20.6	32	1	US-08-305-799A-2	Sequence 2, Appli
433	7	20.6	34	1	US-07-915-247A-23	Sequence 23, Appl
434	7	20.6	34	1	US-07-915-247A-24	Sequence 24, Appl
435	7	20.6	34	1	US-08-443-863-23	Sequence 23, Appl
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440	7	20.6	34	1	US-08-468-275-8	Sequence 8, Appli
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452	7	20.6	34	2	US-08-477-022-36	Sequence 36, Appl
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454	7	20.6	34	2	US-08-449-447-24	Sequence 24, Appl
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456	7	20.6	34	2	US-08-449-447-36	Sequence 36, Appl
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460	7	20.6	34	2	US-08-184-328-36	Sequence 36, Appl
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462	7	20.6	34	2	US-08-521-097-24	Sequence 24, Appl
463	7	20.6	34	2	US-08-521-097-35	Sequence 35, Appl
464	7	20.6	34	2	US-08-521-097-36	Sequence 36, Appl
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466	7	20.6	34	4	US-09-007-466-8	Sequence 8, Appli
467	7	20.6	35	2	US-08-142-551B-10	Sequence 10, Appl

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470	7	20.6	35	4	US-08-952-980B-8	Sequence 8, Appli
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494	6	17.6	31	4	US-09-442-989-14	Sequence 14, Appl
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533	4	11.8	30	1	US-08-305-799A-3	Sequence 3, Appli
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535	4	11.8	30	4	US-09-205-258-821	Sequence 821, App
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544	4	11.8	31	1	US-08-198-094-62	Sequence 62, Appl
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553	4	11.8	31	3	US-08-107-794A-62	Sequence 62, Appl
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557	4	11.8	31	5	PCT-US93-07424-50	Sequence 50, Appl
558	4	11.8	31	5	PCT-US93-07424-62	Sequence 62, Appl
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565	4	11.8	32	1	US-08-190-802A-183	Sequence 183, App
566	4	11.8	32	1	US-08-190-802A-216	Sequence 216, App
567	4	11.8	32	3	US-08-477-346-110	Sequence 110, App
568	4	11.8	32	3	US-08-477-346-114	Sequence 114, App
569	4	11.8	32	3	US-08-477-346-183	Sequence 183, App
570	4	11.8	32	3	US-08-477-346-216	Sequence 216, App
571	4	11.8	32	4	US-08-473-089-110	Sequence 110, App
572	4	11.8	32	4	US-08-473-089-114	Sequence 114, App
573	4	11.8	32	4	US-08-473-089-183	Sequence 183, App
574	4	11.8	32	4	US-08-473-089-216	Sequence 216, App
575	4	11.8	32	4	US-09-149-476-442	Sequence 442, App
576	4	11.8	32	4	US-08-487-072A-110	Sequence 110, App
577	4	11.8	32	4	US-08-487-072A-114	Sequence 114, App
578	4	11.8	32	4	US-08-487-072A-183	Sequence 183, App
579	4	11.8	32	4	US-08-487-072A-216	Sequence 216, App
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585	4	11.8	33	4	US-09-205-258-368	Sequence 368, App
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587	4	11.8	34	1	US-07-956-700B-7	Sequence 7, Appli
588	4	11.8	34	1	US-08-476-537-7	Sequence 7, Appli
589	4	11.8	34	1	US-08-485-607-7	Sequence 7, Appli
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592	4	11.8	35	1	US-08-463-660-6	Sequence 6, Appli
593	4	11.8	35	1	US-08-678-280-6	Sequence 6, Appli
594	4	11.8	35	4	US-09-227-357-486	Sequence 486, App
595	4	11.8	35	4	US-09-690-454-138	Sequence 138, App
596	4	11.8	36	1	US-08-477-727A-104	Sequence 104, App
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600	4	11.8	37	1	US-08-231-730A-45	Sequence 45, Appl
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604	4	11.8	37	1	US-08-477-727A-105	Sequence 105, App
605	4	11.8	37	1	US-08-477-727A-106	Sequence 106, App
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615	4	11.8	37	2	US-08-961-716-12	Sequence 12, Appl
616	4	11.8	37	2	US-08-505-486-50	Sequence 50, Appl
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625	4	11.8	37	3	US-09-340-154-50	Sequence 50, Appl
626	4	11.8	37	3	US-08-302-069A-23	Sequence 23, Appl
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634	4	11.8	37	4	US-09-758-318-16	Sequence 16, Appl
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636	4	11.8	37	5	PCT-US95-09338-50	Sequence 50, Appl
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683	3	8.8	28	1	US-07-690-300B-78	Sequence 78, Appl
684	3	8.8	28	1	US-07-690-300B-79	Sequence 79, Appl
685	3	8.8	28	1	US-07-690-300B-82	Sequence 82, Appl
686	3	8.8	28	1	US-07-690-300B-88	Sequence 88, Appl
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688	3	8.8	28	1	US-07-690-300B-93	Sequence 93, Appl
689	3	8.8	28	1	US-07-663-413-29	Sequence 29, Appl
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692	3	8.8	28	1	US-07-833-468-1	Sequence 1, Appli
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697	3	8.8	28	1	US-08-201-092-2	Sequence 2, Appli
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701	3	8.8	28	1	US-07-966-187-2	Sequence 2, Appli
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703	3	8.8	28	1	US-07-924-054-11	Sequence 11, Appl
704	3	8.8	28	1	US-08-243-082-1	Sequence 1, Appli
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706	3	8.8	28	1	US-08-246-572-5	Sequence 5, Appli
707	3	8.8	28	1	US-08-190-802A-84	Sequence 84, Appl
708	3	8.8	28	1	US-08-361-443-1	Sequence 1, Appli
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713	3	8.8	28	1	US-08-311-611A-195	Sequence 195, App
714	3	8.8	28	1	US-08-311-611A-196	Sequence 196, App
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717	3	8.8	28	1	US-08-194-591-1	Sequence 1, Appli
718	3	8.8	28	1	US-08-194-591-2	Sequence 2, Appli
719	3	8.8	28	1	US-08-257-446-6	Sequence 6, Appli
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723	3	8.8	28	1	US-08-372-783-194	Sequence 194, App
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725	3	8.8	28	1	US-08-372-783-196	Sequence 196, App
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731	3	8.8	28	1	US-07-977-630-47	Sequence 47, Appl
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738	3	8.8	28	1	US-08-372-105-194	Sequence 194, App
739	3	8.8	28	1	US-08-372-105-195	Sequence 195, App
740	3	8.8	28	1	US-08-372-105-196	Sequence 196, App
741	3	8.8	28	1	US-08-306-473A-12	Sequence 12, Appl
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743	3	8.8	28	1	US-08-306-473A-193	Sequence 193, App
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746	3	8.8	28	1	US-08-306-473A-196	Sequence 196, App
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752	3	8.8	28	1	US-08-308-729-5	Sequence 5, Appli



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788	3	8.8	28	1	US-08-308-729-45	Sequence 45, Appl
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794	3	8.8	28	1	US-08-308-729-53	Sequence 53, Appl
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807	3	8.8	28	1	US-08-308-729-71	Sequence 71, Appl
808	3	8.8	28	1	US-08-308-729-72	Sequence 72, Appl
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842	3	8.8	28	2	US-08-621-803-142	Sequence 142, App
843	3	8.8	28	2	US-08-621-803-143	Sequence 143, App
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847	3	8.8	28	2	US-08-485-445A-194	Sequence 194, App
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849	3	8.8	28	2	US-08-485-445A-196	Sequence 196, App
850	3	8.8	28	2	US-08-621-259A-5	Sequence 5, Appli
851	3	8.8	28	2	US-08-621-259A-110	Sequence 110, App
852	3	8.8	28	2	US-08-621-259A-111	Sequence 111, App
853	3	8.8	28	2	US-08-621-259A-113	Sequence 113, App
854	3	8.8	28	2	US-08-621-259A-114	Sequence 114, App
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861	3	8.8	28	2	US-08-620-151-129	Sequence 129, App
862	3	8.8	28	2	US-08-398-590A-43	Sequence 43, Appl
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869	3	8.8	28	2	US-08-475-985-19	Sequence 19, Appl
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872	3	8.8	28	2	US-08-413-708B-8	Sequence 8, Appli
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874	3	8.8	28	2	US-08-691-814B-73	Sequence 73, Appl
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877	3	8.8	28	2	US-08-897-624-2	Sequence 2, Appli
878	3	8.8	28	3	US-09-110-953-8	Sequence 8, Appli
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887	3	8.8	28	3	US-08-484-223B-84	Sequence 84, Appl
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913	3	8.8	28	3	US-08-919-597-84	Sequence 84, Appl
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937	3	8.8	28	3	US-08-657-162-12	Sequence 12, Appl
938	3	8.8	28	3	US-08-657-162-56	Sequence 56, Appl
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941	3	8.8	28	3	US-08-657-162-195	Sequence 195, App
942	3	8.8	28	3	US-08-657-162-196	Sequence 196, App
943	3	8.8	28	3	US-09-433-428D-62	Sequence 62, Appl
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958	3	8.8	28	3	US-08-817-811-66	Sequence 66, Appl
959	3	8.8	28	3	US-08-817-811-67	Sequence 67, Appl
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964	3	8.8	28	3	US-08-985-499-39	Sequence 39, Appl
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967	3	8.8	28	3	US-09-066-046-19	Sequence 19, Appl
968	3	8.8	28	3	US-09-253-396A-223	Sequence 223, App
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970	3	8.8	28	3	US-09-093-539-12	Sequence 12, Appl
971	3	8.8	28	3	US-09-093-539-56	Sequence 56, Appl
972	3	8.8	28	3	US-08-485-264A-84	Sequence 84, Appl
973	3	8.8	28	3	US-08-485-264A-136	Sequence 136, App
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980	3	8.8	28	3	US-09-041-886-42	Sequence 42, Appl

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983	3	8.8	28	3	US-09-041-886-53	Sequence 53, Appl
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985	3	8.8	28	3	US-09-041-886-56	Sequence 56, Appl
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987	3	8.8	28	3	US-07-966-049A-9	Sequence 9, Appli
988	3	8.8	28	3	US-08-995-369-1	Sequence 1, Appli
989	3	8.8	28	3	US-09-171-654-1	Sequence 1, Appli
990	3	8.8	28	3	US-08-605-430-43	Sequence 43, Appl
991	3	8.8	28	3	US-08-894-327-22	Sequence 22, Appl
992	3	8.8	28	3	US-09-082-279B-54	Sequence 54, Appl
993	3	8.8	28	3	US-09-082-279B-62	Sequence 62, Appl
994	3	8.8	28	3	US-09-082-279B-982	Sequence 982, App
995	3	8.8	28	3	US-09-082-279B-1279	Sequence 1279, Ap
996	3	8.8	28	3	US-09-082-279B-1280	Sequence 1280, Ap
997	3	8.8	28	3	US-09-082-279B-1314	Sequence 1314, Ap
998	3	8.8	28	3	US-09-082-279B-1315	Sequence 1315, Ap
999	3	8.8	28	3	US-08-477-346-84	Sequence 84, Appl
1000	3	8.8	28	3	US-08-942-046-34	Sequence 34, Appl

#### ALIGNMENTS

#### RESULT 1

US-07-765-373-1

; Sequence 1, Application US/07765373

; Patent No. 5393869

#### ; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: KAWASE, Masahiro

; APPLICANT: YAMAZAKI, Iwao

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES

; NUMBER OF SEQUENCES: 2

#### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; ADDRESSEE: CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

#### ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

#### ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/765,373

; FILING DATE: 19910925

; CLASSIFICATION: 530

#### ; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, Gregory D.

; REGISTRATION NUMBER: 30901

; REFERENCE/DOCKET NUMBER: 41289

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)523-3400  
; TELEFAX: (617)523-6440  
; TELEX: 20091 STRE UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
US-07-765-373-1

Query Match 100.0%; Score 34; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

US-08-033-099-1

; Sequence 1, Application US/08033099  
; Patent No. 5434246

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko  
; APPLICANT: NAKAGAWA, Shizue  
; APPLICANT: TAKETOMI, Shigehisa  
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID G.CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/033,099  
; FILING DATE: 19930316  
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, Gregory D  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: 42528

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400  
; TELEFAX: (613)523-6440  
; TELEX: 200291 STRE UR

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal  
US-08-033-099-1

Query Match 100.0%; Score 34; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

US-08-262-495C-1

; Sequence 1, Application US/08262495C  
; Patent No. 5556940  
; GENERAL INFORMATION:  
; APPLICANT: WILICK, Gordon E.  
; APPLICANT: WHITFIELD, James F.  
; APPLICANT: SUREWICZ, Witold  
; APPLICANT: SUNG, Wing L.  
; APPLICANT: NEUGENBAUER, Witold  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kirby, Eades, Gale, Baker  
; STREET: 112 Kent Street, Suite 770,  
; CITY: Ottawa  
; COUNTRY: Canada  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/262,495C  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EADES, No. 5556940ris M.  
; REGISTRATION NUMBER: 5,263  
; REFERENCE/DOCKET NUMBER: 36210  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613)-237-6900  
; TELEFAX: (613)-237-0045  
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-262-495C-1

Query Match 100.0%; Score 34; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 4

US-07-915-247A-1

; Sequence 1, Application US/07915247A  
; Patent No. 5589452  
; GENERAL INFORMATION:  
; APPLICANT: Krstenansky, John L.  
; APPLICANT: Nestor Jr., John J.  
; APPLICANT: Ho, Teresa H.  
; APPLICANT: Vickery, Brian H.  
; APPLICANT: Bach, Chinh T.  
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND  
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.  
; STREET: 3401 Hillview Ave.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/915,247A  
; FILING DATE: 19920714  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schmonsees, William  
; REGISTRATION NUMBER: 31,796  
; REFERENCE/DOCKET NUMBER: 27610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-6593  
; TELEFAX: 415-496-3529  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid







; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
US-08-448-070-1

Query Match 100.0%; Score 34; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

US-08-488-105-7

; Sequence 7, Application US/08488105

; Patent No. 5717062

; GENERAL INFORMATION:

; APPLICANT: Chorev, Michael

; APPLICANT: Rosenblatt, Michael

; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,105

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Tsao, Y. Rocky

; REGISTRATION NUMBER: 34,053

; REFERENCE/DOCKET NUMBER: 00537/112001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; OTHER INFORMATION: The side chains of Lys at

; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an amide bond,

; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,  
CONH2), rather  
; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).  
US-08-488-105-7

Query Match 100.0%; Score 34; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-08-468-275-6

; Sequence 6, Application US/08468275

; Patent No. 5747453

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94303-0802

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,275

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLER, D. BYRON

; REGISTRATION NUMBER: 30,661

; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 496-8150

; TELEFAX: (415) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-468-275-6

Query Match 100.0%; Score 34; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

US-08-449-500-1

; Sequence 1, Application US/08449500

; Patent No. 5798225

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,500

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-449-500-1

Query Match 100.0%; Score 34; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 10

US-08-449-317A-1

; Sequence 1, Application US/08449317A

; Patent No. 5807823

; GENERAL INFORMATION:

; APPLICANT: Vickery, Brian H.

; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID

; TITLE OF INVENTION: INDUCED OSTEOPENIA

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,317A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-449-317A-1

Query Match 100.0%; Score 34; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 11

US-08-142-551B-2

; Sequence 2, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,551B  
; FILING DATE: 25-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/077,296  
; FILING DATE: 14-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/898,219  
; FILING DATE: 12-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,677  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-7400  
; TELEFAX: (415) 854-8275  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..34  
; OTHER INFORMATION: /note= "The sequence of the 34  
; OTHER INFORMATION: amino acid truncated human PTH peptide,  
; OTHER INFORMATION: designated: Human PTH."

US-08-142-551B-2

Query Match 100.0%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 12

US-08-477-022-1

; Sequence 1, Application US/08477022  
; Patent No. 5821225  
; GENERAL INFORMATION:  
; APPLICANT: Vickery, Brian H.  
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID  
; TITLE OF INVENTION: INDUCED OSTEOPENIA  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.  
; STREET: 3401 Hillview Ave.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,022  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schmonsees, William  
; REGISTRATION NUMBER: 31,796  
; REFERENCE/DOCKET NUMBER: 27610-P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-6593  
; TELEFAX: 415-496-3529  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
US-08-477-022-1

Query Match 100.0%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||



Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

US-08-449-447-1

; Sequence 1, Application US/08449447  
; Patent No. 5840837  
; GENERAL INFORMATION:  
; APPLICANT: Krstenansky, John L.  
; APPLICANT: Nestor Jr., John J.  
; APPLICANT: Ho, Teresa H.  
; APPLICANT: Vickery, Brian H.  
; APPLICANT: Bach, Chinh T.  
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND  
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.  
; STREET: 3401 Hillview Ave.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,447  
; FILING DATE: 18-JAN-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schmonsees, William  
; REGISTRATION NUMBER: 31,796  
; REFERENCE/DOCKET NUMBER: 27610-P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-6593  
; TELEFAX: 415-496-3529  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal

US-08-449-447-1

Query Match 100.0%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

US-08-835-231-13

; Sequence 13, Application US/08835231

; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 5861284uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

; APPLICATION NUMBER: JP 024841

; FILING DATE: 19-FEB-1991

; APPLICATION NUMBER: JP 0271438

; FILING DATE: 18-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41614-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal





; MOLECULE TYPE: protein  
US-08-411-726-2

Query Match 100.0%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-08-691-647C-5

; Sequence 5, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue, 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C

; FILING DATE: August 2, 1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-691-647C-5

Query Match 100.0%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18

; Sequence 1, Application US/08521097

; GENERAL INFORMATION:

APPLICANT: Nestor Jr., John J.

APPLICANT: Vickery, Brian H.

APPLICANT: Bach, Chinh T.

TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

STREET: 3401 Hillview Ave.

CITY: Palo Alto

; STATE: CA

COUNTRY: USA

ZIP: 94303

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/521,097

FILING DATE: 29-AUG-1995

CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/184,328

FILING DATE: 18-JAN-1994

; ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-6593

TELEFAX: 415-496-3529

; INFORMATION FOR SEO ID NO: 1:

SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

```
;      TOPOLOGY:  linear
```

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal  
US-08-521-097-1

Query Match 100.0%; Score 34; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-09-044-536A-1

; Sequence 1, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

APPLICANT: FUKUDA, Tsunehiko

APPLICANT: NAKAGAWA, Shizue

APPLICANT: HABASHITA, Junko

APPLICANT: TAKETOMI, Shigehisa

10 TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 Water Street

CITY: Boston

; STATE: Massachusetts

COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

```
;      COMPUTER:  IBM PC compatible
```

; OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/662,871

FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 46509-DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400

TELEFAX: (617) 523-6440

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

```
; MOLECULE TYPE: peptide
```

; FEATURE:

```
; NAME/KEY: partial peptide
```

; LOCATION: 1..34  
US-09-044-536A-1

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

US-08-904-760B-22

; Sequence 22, Application US/08904760B

; Patent No. 6110892

; GENERAL INFORMATION:

; APPLICANT: Jean-Rene, Barbier

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE

; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 No. 6110892th Glebe Rd. 8th floor

; CITY: Arlington

; STATE: VA

; COUNTRY: USA

; ZIP: 22201-4741

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/904,760B

; FILING DATE: 01-AUG-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/691,647

; FILING DATE: 02-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1339-6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-816-4000

; TELEFAX: 703-816-4100

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear



; MOLECULE TYPE: protein  
US-08-904-760B-22

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-09-108-661-13

; Sequence 13, Application US/09108661

; Patent No. 6287806

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 6287806uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/108,661

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

; APPLICATION NUMBER: JP 024841

; FILING DATE: 19-FEB-1991

; APPLICATION NUMBER: JP 0271438

; FILING DATE: 18-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41614-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-09-108-661-13

Query Match 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 22

US-09-007-466-6

; Sequence 6, Application US/09007466  
; Patent No. 6313092

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.  
; APPLICANT: OLDENBURG, KEVIN R.  
; TITLE OF INVENTION: METHOD FOR INCREASING THE  
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ALZA CORPORATION  
; STREET: 950 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94303-0802

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/007,466  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/468,275  
; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLER, D. BYRON  
; REGISTRATION NUMBER: 30,661  
; REFERENCE/DOCKET NUMBER: O360-0002; ARC-2349

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 496-8150

; TELEFAX: (415) 496-8048  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-007-466-6

Query Match 100.0%; Score 34; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

US-09-406-813-1

; Sequence 1, Application US/09406813  
; Patent No. 6316410  
; GENERAL INFORMATION:  
; APPLICANT: Barbier, Jean-Rene  
; APPLICANT: Morley, Paul  
; APPLICANT: Whitfield, James  
; APPLICANT: Willick, Gordon E.  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF  
; TITLE OF INVENTION: OSTEOPOROSIS  
; FILE REFERENCE: 10688-1B  
; CURRENT APPLICATION NUMBER: US/09/406,813  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/904,760  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-406-813-1

Query Match 100.0%; Score 34; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

US-08-952-980B-6

; Sequence 6, Application US/08952980B  
; Patent No. 6333189  
; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.  
 ; APPLICANT: OLDENBURG, KEVIN R.  
 ; TITLE OF INVENTION: METHOD FOR INCREASING THE  
 ; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ALZA CORPORATION  
 ; STREET: 950 PAGE MILL ROAD  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94303-0802  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/952,980B  
 ; FILING DATE: 20-NOV-1997  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MILLER, D. BYRON  
 ; REGISTRATION NUMBER: 30,661  
 ; REFERENCE/DOCKET NUMBER: 2349 CIP 1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 496-8150  
 ; TELEFAX: (650) 496-8048  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 34 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-952-980B-6

Query Match 100.0%; Score 34; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 25

US-09-228-990-1

; Sequence 1, Application US/09228990  
 ; Patent No. 6472505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Condon, Stephen M.  
 ; APPLICANT: Morize, Isabelle  
 ; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.

```

; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,990
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-09-228-990-1

```

```

Query Match          100.0%; Score 34; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

# RESULT 26

US-09-447-800-8

```

; Sequence 8, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152

```

US-09-447-800-8

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLODVHNF 34

## RESULT 27

US-09-536-785A-22

```
; Sequence 22, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-536-785A-22
```

Query Match 100.0%; Score 34; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 28

US-09-442-989-26

; Sequence 26, Application US/09442989  
; Patent No. 6569993  
; GENERAL INFORMATION:  
; APPLICANT: Sledeski, Adam W.  
; APPLICANT: Mencil, James J.  
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: A3113B-US  
; CURRENT APPLICATION NUMBER: US/09/442,989  
; CURRENT FILING DATE: 1999-11-18  
; EARLIER APPLICATION NUMBER: 60/081,897  
; EARLIER FILING DATE: 1998-04-15  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
US-09-442-989-26

Query Match 100.0%; Score 34; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.4e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 29

PCT-US95-15800-22

; Sequence 22, Application PC/TUS9515800  
; GENERAL INFORMATION:  
; APPLICANT: BioNebraska, Inc.  
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING  
; TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRICTS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 Norwest Center, 90 S. 7th Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: U.S.A.  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15800
; FILING DATE: 07-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,530
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.45USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
PCT-US95-15800-22

```

```

Query Match          100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 30

US-08-256-363-3

; Sequence 3, Application US/08256363

; Patent No. 5783558

; GENERAL INFORMATION:

; APPLICANT: DUVOS, CHRISTIAN

; APPLICANT: MAYER, HUBERT

; APPLICANT: MUELLER-BECKMANN, BERND

; APPLICANT: STREIN, KLAUS

; APPLICANT: WINGENDER, EDGAR

; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR

; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIKAIDO, MARMELESTEIN, MURRAY, AND ORAM

; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 2005 5701



```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,363
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 03 040.4
; FILING DATE: 04-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00259
; FILING DATE: 04-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KLESNER, SHARON N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: P1614-4025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-363-3

```

```

Query Match          100.0%; Score 34; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 5.5e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        |||||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 31

US-08-256-363-4

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; Sequence 4, Application US/08256363
; Patent No. 5783558
; GENERAL INFORMATION:
; APPLICANT: DUVOS, CHRISTIAN
; APPLICANT: MAYER, HUBERT
; APPLICANT: MUELLER-BECKMANN, BERND
; APPLICANT: STREIN, KLAUS
; APPLICANT: WINGENDER, EDGAR
; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR
; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARCELSTEIN, MURRAY, AND ORAM
; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY
; CITY: WASHINGTON

```

; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 2005 5701  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/256,363  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE P 42 03 040.4  
 ; FILING DATE: 04-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP93/00259  
 ; FILING DATE: 04-FEB-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KLESNER, SHARON N.  
 ; REGISTRATION NUMBER: 36,335  
 ; REFERENCE/DOCKET NUMBER: P1614-4025  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 638-5000  
 ; TELEFAX: (202) 638-4810  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 36 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-256-363-4

Query Match 100.0%; Score 34; DB 1; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-25;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
 |||||  
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

# RESULT 32

US-08-440-117-1

; Sequence 1, Application US/08440117

; Patent No. 5744444

## ; GENERAL INFORMATION:

; APPLICANT: Forssmann, Wolf-Georg

; APPLICANT: Herbst, Franz

; APPLICANT: Schulz-Knappe, Peter

; APPLICANT: Adermann, Knut

; APPLICANT: Gagelmann, Michael

; TITLE OF INVENTION: hPTH-FRAGMENT-(1-37), THE PREPARATION

; TITLE OF INVENTION: THEREOF, MEDICAMENTS CONTAINING SAME AND THE USE THEREOF

; NUMBER OF SEQUENCES: 1

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,117
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,658
; FILING DATE:
; APPLICATION NUMBER: 07/863,291
; FILING DATE: 06-JUN-1992
; APPLICATION NUMBER: DE p3935738.4
; FILING DATE: 27-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP90/01807
; FILING DATE: 25-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Helmuth A
; REGISTRATION NUMBER: 17,033
; REFERENCE/DOCKET NUMBER: P-9650-23333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-440-117-1

```

```

Query Match          100.0%; Score 34; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.8e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        |||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

```

RESULT 33
US-09-068-738A-16

```

```

; Sequence 16, Application US/09068738A
; Patent No. 6136564
; GENERAL INFORMATION:
;   APPLICANT: KOPETZKI, Erhard
;   TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF PEPTIDES VIA
;   TITLE OF INVENTION: STREPTAVIDIN FUSION PROTEINS
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: ARENT FOX KINTNER PLOTKIN & KAHN
;     STREET: 1050 CONNECTICUT AVENUE, NW, SUITE 600
;     CITY: Washington
;     STATE: DC
;     COUNTRY: USA
;     ZIP: 20036-5339
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/068,738A
;     FILING DATE: June 25, 1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/EP 96/04850
;     FILING DATE: 11-NOV-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Berman, Richard J.
;     REGISTRATION NUMBER: 39,107
;     REFERENCE/DOCKET NUMBER: P108341-08035
;   INFORMATION FOR SEQ ID NO: 16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 37 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-09-068-738A-16

```

```

Query Match          100.0%; Score 34; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.8e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

# RESULT 34

US-08-112-024-1

```

; Sequence 1, Application US/08112024
; Patent No. 5578567
; GENERAL INFORMATION:
;   APPLICANT: Cardinaux, Francois
;   APPLICANT: Oechslein, Christine
;   APPLICANT: Rummelt, Andreas
;   TITLE OF INVENTION: Nasal Pharmaceutical Composition
;   NUMBER OF SEQUENCES: 2

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Sandoz Corporation
;   STREET:  59 Route 10
;   CITY:  East Hanover
;   STATE:  New Jersey
;   COUNTRY:  U.S.A.
;   ZIP:  07936
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/112,024
;   FILING DATE:  25-AUG-1993
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/028,852
;   FILING DATE:  10-MAR-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/948,366
;   FILING DATE:  21-SEP-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/762,825
;   FILING DATE:  19-SEP-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  GB 9020544
;   FILING DATE:  20-SEP-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Battle, Carl W
;   REGISTRATION NUMBER:  30,731
;   REFERENCE/DOCKET NUMBER:  100-7639/CONT3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  201-503-8177
;   TELEFAX:  201-503-8807
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  38 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  38
;   OTHER INFORMATION:  /note= "This terminal glycine ends
;   OTHER INFORMATION:  either with a normal carboxy group or with an
;   OTHER INFORMATION:  amide group."
US-08-112-024-1

```

```

Query Match          100.0%;  Score 34;  DB 1;  Length 38;
Best Local Similarity 100.0%;  Pred. No. 5.9e-25;
Matches  34;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

Db

|||||  
1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

US-08-232-849-1

; Sequence 1, Application US/08232849

; Patent No. 5607915

; GENERAL INFORMATION:

; APPLICANT: Patton, John S.

; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments

; TITLE OF INVENTION: of Parathyroid Hormone

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,849

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/953,397

; FILING DATE: 29-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15225-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-232-849-1

Query Match 100.0%; Score 34; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 5.9e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

US-08-625-586-1

```
; Sequence 1, Application US/08625586
; Patent No. 5814607
; GENERAL INFORMATION:
;   APPLICANT: Patton, John S.
;   TITLE OF INVENTION: Pulmonary Delivery of Active Fragments
;   TITLE OF INVENTION: of Parathyroid Hormone
;   NUMBER OF SEQUENCES: 1
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/625,586
;     FILING DATE: 27-MAR-1996
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/232,849
;     FILING DATE: 25-APR-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/953,397
;     FILING DATE: 29-SEP-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Heslin, James M.
;     REGISTRATION NUMBER: 29,541
;     REFERENCE/DOCKET NUMBER: 15225-000310
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-576-0200
;     TELEFAX: 415-576-0300
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 38 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-625-586-1
```

```
Query Match          100.0%; Score 34; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.9e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 37

US-09-128-401-1  
; Sequence 1, Application US/09128401  
; Patent No. 6080721  
; GENERAL INFORMATION:  
; APPLICANT: Patton, John S.  
; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments  
; TITLE OF INVENTION: of Parathyroid Hormone  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,401  
; FILING DATE: 03-AUG-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/953,397  
; FILING DATE: 29-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,849  
; FILING DATE: 25-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/625,586  
; FILING DATE: 28-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heslin, James M.  
; REGISTRATION NUMBER: 29,541  
; REFERENCE/DOCKET NUMBER: 015225-000330US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-128-401-1

Query Match 100.0%; Score 34; DB 3; Length 38;  
Best Local Similarity 100.0%; Pred. No. 5.9e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34



RESULT 38

US-09-447-800-9

```
; Sequence 9, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
```

US-09-447-800-9

```
Query Match          97.1%; Score 33; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.4e-24;
Matches    33; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33
          ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33
```

RESULT 39

US-08-903-497A-1

```
; Sequence 1, Application US/08903497A
; Patent No. 6147186
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: J ppner, Harald
; TITLE OF INVENTION: No. 6147186el Parathyroid Hormone-Related
; TITLE OF INVENTION: Peptide Analogs
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/903,497A
;   FILING DATE:  30-JUL-1997
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 60/025,471
;   FILING DATE:  31-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Markowicz, Karen R.
;   REGISTRATION NUMBER:  36,351
;   REFERENCE/DOCKET NUMBER:  0609.4310001/JAG/KRM
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (202) 371-2600
;   TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  34 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  not relevant
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  MODIFIED-SITE
;   LOCATION:  34
;   OTHER INFORMATION:  CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
;   OTHER INFORMATION:  AMIDE
US-08-903-497A-1

```

```

Query Match          97.1%;  Score 33;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 4.5e-24;
Matches  33;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33
        ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

```

RESULT 40

US-09-635-076-1

```

; Sequence 1, Application US/09635076
; Patent No. 6362163
; GENERAL INFORMATION:
; APPLICANT:  Gardella, Thomas J.
; APPLICANT:  J ppner, Harald
; TITLE OF INVENTION:  No. 6362163el Parathyroid Hormone-Related
; TITLE OF INVENTION:  Peptide Analogs
; NUMBER OF SEQUENCES:  7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET:  1100 New York Avenue, N.W., Suite 600
; CITY:  Washington
; STATE:  DC
; COUNTRY:  USA
; ZIP:  20005
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/635,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/903,497
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
; OTHER INFORMATION: AMIDE
US-09-635-076-1

```

```

Query Match          97.1%; Score 33; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33
        ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

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Search completed: January 14, 2004, 10:43:28
Job time : 16.5452 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 10.0623 Seconds  
 (without alignments)  
 324.949 Million cell updates/sec

Title: US-09-843-221A-161  
 Perfect score: 34  
 Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28  
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR\_76:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	14.7	34	2	A84241	hypothetical prote
2	5	14.7	34	2	B97032	transcription regu
3	5	14.7	35	2	E95098	hypothetical prote
4	4	11.8	28	2	T09594	gene LFY protein -
5	4	11.8	29	1	A55527	pyrroloquinoline q
6	4	11.8	29	2	S01614	dystrophin - rat (
7	4	11.8	29	2	I78537	copper transportin
8	4	11.8	29	2	S78412	ribosomal protein
9	4	11.8	30	2	S63531	hypothetical prote
10	4	11.8	31	2	S44471	glucagon G1 - Nort
11	4	11.8	31	2	S44472	glucagon G2 - Nort
12	4	11.8	31	2	D70236	hypothetical prote
13	4	11.8	32	2	F23454	ovalbumin phosphos

14	4	11.8	32	2	D31461	T-cell receptor de
15	4	11.8	32	2	G84161	hypothetical prote
16	4	11.8	33	2	E81714	hypothetical prote
17	4	11.8	35	2	D23454	ovalbumin phosphos
18	4	11.8	35	2	G23454	ovalbumin phosphos
19	4	11.8	35	2	D82125	hypothetical prote
20	4	11.8	36	2	S70806	hypothetical prote
21	4	11.8	36	2	F95057	hypothetical prote
22	4	11.8	36	2	A84774	hypothetical prote
23	4	11.8	36	2	S46227	hypothetical prote
24	4	11.8	37	2	S71912	hemoglobin, extrac
25	4	11.8	37	2	T12635	homeotic protein H
26	4	11.8	39	1	CKFHCS	sarcotoxin IC - fl
27	4	11.8	39	2	S71913	hemoglobin, extrac
28	4	11.8	39	2	S77164	ycf32 protein - Sy
29	3	8.8	28	2	A42272	brain-type creatin
30	3	8.8	28	2	C32416	phospholipase A2 (
31	3	8.8	28	2	B60071	vasoactive intesti
32	3	8.8	28	2	A60304	vasoactive intesti
33	3	8.8	28	2	S58386	T-cell receptor be
34	3	8.8	28	2	PN0047	signal transductio
35	3	8.8	28	2	S56121	type I DNA methylt
36	3	8.8	28	2	S70894	hypothetical prote
37	3	8.8	28	2	S22469	hypothetical prote
38	3	8.8	28	2	S26254	rel protein - chic
39	3	8.8	28	2	I59477	antigen, T-cell re
40	3	8.8	28	2	F46522	T-cell receptor et
41	3	8.8	28	2	H85908	hypothetical prote
42	3	8.8	29	1	GCCB	glucagon - Chinch
43	3	8.8	29	2	S39968	probable hydro-lya
44	3	8.8	29	2	A61509	islet amyloid poly
45	3	8.8	29	2	S17147	galanin - chicken
46	3	8.8	29	2	T44245	ribosomal protein
47	3	8.8	29	2	A05272	gelsolin, cytosoli
48	3	8.8	29	2	B44101	calmodulin, vasoac
49	3	8.8	29	2	S42642	probable rhicadhes
50	3	8.8	29	2	A00774	3-oxoadipate enol-
51	3	8.8	29	2	B81136	hypothetical prote
52	3	8.8	29	2	I84189	cyclic AMP recepto
53	3	8.8	29	2	S65747	CDP-paratose synth
54	3	8.8	29	2	S65748	CDP-paratose synth
55	3	8.8	29	2	B41476	probable antigen 2
56	3	8.8	29	2	S68094	2,3-dihydroxybenzo
57	3	8.8	29	2	A27688	mammary-derived gr
58	3	8.8	29	2	T31443	cytochrome bc chai
59	3	8.8	29	2	F85570	hypothetical prote
60	3	8.8	29	2	I49732	NADH2 dehydrogenas
61	3	8.8	29	2	A59479	NADP phosphatase I
62	3	8.8	30	2	S40309	tyrosine 3-monooxy
63	3	8.8	30	2	C21897	ornithine carbamoy
64	3	8.8	30	2	A28562	glutathione transf
65	3	8.8	30	2	A05315	pancreatic ribonuc
66	3	8.8	30	2	A44598	endo-1,4-beta-xyla
67	3	8.8	30	2	A61333	trypsin (EC 3.4.21
68	3	8.8	30	2	S21815	H+-exporting ATPas
69	3	8.8	30	2	A44912	cysteine proteinas
70	3	8.8	30	2	B61125	glucagon-like pept

71	3	8.8	30	2	C61125	glucagon-like pept
72	3	8.8	30	2	F32502	T-cell receptor de
73	3	8.8	30	2	PD0013	cAMP response elem
74	3	8.8	30	2	S11617	ribosomal protein
75	3	8.8	30	2	S21195	spectrin beta chai
76	3	8.8	30	2	PC4172	profilin - rat (fr
77	3	8.8	30	2	A34461	heat shock protein
78	3	8.8	30	2	A22977	delta-endotoxin -
79	3	8.8	30	2	A44913	34K core flagella
80	3	8.8	30	2	S08565	ribulose-bisphosph
81	3	8.8	30	2	S30333	N-carbamoyl-D-amin
82	3	8.8	30	2	PQ0444	hypothetical prote
83	3	8.8	30	2	B95020	hypothetical prote
84	3	8.8	30	2	H95021	hypothetical prote
85	3	8.8	30	2	D72276	hypothetical prote
86	3	8.8	30	2	D70253	conserved hypothet
87	3	8.8	30	2	B70165	hypothetical prote
88	3	8.8	30	2	B81956	hypothetical prote
89	3	8.8	30	2	E82294	hypothetical prote
90	3	8.8	30	2	D82251	hypothetical prote
91	3	8.8	30	2	S72626	small-cell-variant
92	3	8.8	30	2	A35687	probable 39K inorg
93	3	8.8	30	2	S73316	photosystem I chai
94	3	8.8	30	2	A32946	trypsin-like serin
95	3	8.8	30	2	PL0189	Ig light chain - s
96	3	8.8	30	2	S65519	carcinoembryonic a
97	3	8.8	30	2	S34765	4-hydroxybutyryl-C
98	3	8.8	30	2	D81532	hypothetical prote
99	3	8.8	30	2	A48923	retrovirus-related
100	3	8.8	30	2	B56586	storage hexamer 2
101	3	8.8	30	2	F81360	very hypothetical
102	3	8.8	30	2	S15650	NADH2 dehydrogenas
103	3	8.8	30	2	H97596	hypothetical prote
104	3	8.8	30	4	I52605	hypothetical MLL/E
105	3	8.8	31	1	A28805	leiurotoxin I [val
106	3	8.8	31	1	A49078	leiurotoxin I-like
107	3	8.8	31	1	S34504	photosystem I prot
108	3	8.8	31	2	T44925	hypothetical prote
109	3	8.8	31	2	S39019	glucagon-like pept
110	3	8.8	31	2	A58793	relaxin chain B -
111	3	8.8	31	2	A58586	conotoxin MrVIA -
112	3	8.8	31	2	F30608	Ig kappa chain V-I
113	3	8.8	31	2	D30608	Ig kappa chain V-I
114	3	8.8	31	2	F31461	T-cell receptor de
115	3	8.8	31	2	S03295	Ig alpha chain C r
116	3	8.8	31	2	S03297	Ig alpha chain C r
117	3	8.8	31	2	I52232	tau protein - huma
118	3	8.8	31	2	A36162	neutrophil-activat
119	3	8.8	31	2	S04980	ferritin heavy cha
120	3	8.8	31	2	S32610	antiviral protein
121	3	8.8	31	2	S38881	inner membrane pro
122	3	8.8	31	2	G95018	hypothetical prote
123	3	8.8	31	2	G95022	hypothetical prote
124	3	8.8	31	2	A95085	hypothetical prote
125	3	8.8	31	2	H95093	hypothetical prote
126	3	8.8	31	2	E95140	hypothetical prote
127	3	8.8	31	2	E95151	hypothetical prote

128	3	8.8	31	2	E70202	hypothetical prote
129	3	8.8	31	2	E70223	hypothetical prote
130	3	8.8	31	2	H70225	hypothetical prote
131	3	8.8	31	2	C70240	hypothetical prote
132	3	8.8	31	2	H70252	hypothetical prote
133	3	8.8	31	2	E64562	hypothetical prote
134	3	8.8	31	2	S49191	hypothetical prote
135	3	8.8	31	2	H82353	hypothetical prote
136	3	8.8	31	2	A05051	hypothetical prote
137	3	8.8	31	2	B23605	histone H1.3 - whe
138	3	8.8	31	2	S78738	protein YOL038c-a
139	3	8.8	31	2	A36221	cecropin P1 - pig
140	3	8.8	31	2	S27112	sarcophilin - rabbi
141	3	8.8	31	2	C84082	hypothetical prote
142	3	8.8	31	2	D81591	hypothetical prote
143	3	8.8	31	2	G81558	hypothetical prote
144	3	8.8	31	2	G82816	hypothetical prote
145	3	8.8	31	2	F82565	hypothetical prote
146	3	8.8	32	1	TCEE	calcitonin - Japan
147	3	8.8	32	1	TCON2	calcitonin 2 - soc
148	3	8.8	32	1	TCON2C	calcitonin 2 - chu
149	3	8.8	32	1	TCON2P	calcitonin 2 - pin
150	3	8.8	32	1	TCON3	calcitonin 3 - coh
151	3	8.8	32	2	S20719	alcohol dehydrogen
152	3	8.8	32	2	A61143	trypsin (EC 3.4.21
153	3	8.8	32	2	D32502	T-cell receptor de
154	3	8.8	32	2	A32502	T-cell receptor de
155	3	8.8	32	2	B40186	ubiquitin / riboso
156	3	8.8	32	2	S57780	histone H3 - rice
157	3	8.8	32	2	A24047	gap junction prote
158	3	8.8	32	2	S51524	anchorin CII - bov
159	3	8.8	32	2	S36809	GTP-binding regula
160	3	8.8	32	2	A29743	translation initia
161	3	8.8	32	2	A03367	lectin - Macrotylo
162	3	8.8	32	2	A44900	fimbrin, SEF 21 -
163	3	8.8	32	2	S03273	photosystem II oxy
164	3	8.8	32	2	C46107	polyomavirus enhan
165	3	8.8	32	2	S08482	regulatory protein
166	3	8.8	32	2	E87694	hypothetical prote
167	3	8.8	32	2	D70222	hypothetical prote
168	3	8.8	32	2	E70225	hypothetical prote
169	3	8.8	32	2	B70241	hypothetical prote
170	3	8.8	32	2	B70257	hypothetical prote
171	3	8.8	32	2	D82353	hypothetical prote
172	3	8.8	32	2	E82279	hypothetical prote
173	3	8.8	32	2	E82089	hypothetical prote
174	3	8.8	32	2	H82416	hypothetical prote
175	3	8.8	32	2	T17394	vrlN protein - Dic
176	3	8.8	32	2	S23476	hypothetical prote
177	3	8.8	32	2	S22304	hypothetical prote
178	3	8.8	32	2	S78323	photosystem II pro
179	3	8.8	32	2	A05015	hypothetical prote
180	3	8.8	32	2	I38619	zinc finger protei
181	3	8.8	32	2	S28398	t-complex protein
182	3	8.8	32	2	T14569	hypothetical prote
183	3	8.8	32	2	H84081	hypothetical prote
184	3	8.8	32	2	F82833	hypothetical prote

185	3	8.8	32	2	JC5802	ovulation stimulat
186	3	8.8	32	2	E85588	hypothetical prote
187	3	8.8	33	2	S43312	2',3'-cyclic-nucle
188	3	8.8	33	2	S26859	chitinase (EC 3.2.
189	3	8.8	33	2	I52219	c-ras-Ki-2 protein
190	3	8.8	33	2	I53221	K-ras protein - hu
191	3	8.8	33	2	PC2300	gaegurin 1 - Korea
192	3	8.8	33	2	I56451	relaxin - hamadrya
193	3	8.8	33	2	E32502	T-cell receptor de
194	3	8.8	33	2	A31461	T-cell receptor de
195	3	8.8	33	2	B31461	T-cell receptor de
196	3	8.8	33	2	A03150	retinoic acid-bind
197	3	8.8	33	2	C46027	neurotransmitter t
198	3	8.8	33	2	PQ0150	dnaK-type molecula
199	3	8.8	33	2	B44906	L1 protein - human
200	3	8.8	33	2	PQ0418	matrix protein M1
201	3	8.8	33	2	S34505	hypothetical prote
202	3	8.8	33	2	G95006	hypothetical prote
203	3	8.8	33	2	C95200	hypothetical prote
204	3	8.8	33	2	A87213	hypothetical prote
205	3	8.8	33	2	F84163	hypothetical prote
206	3	8.8	33	2	E82135	hypothetical prote
207	3	8.8	33	2	H82475	hypothetical prote
208	3	8.8	33	2	S68096	lactate dehydrogen
209	3	8.8	33	2	E82526	hypothetical prote
210	3	8.8	33	2	G85600	hypothetical prote
211	3	8.8	33	2	H85651	hypothetical prote
212	3	8.8	33	2	AC1012	hypothetical prote
213	3	8.8	33	2	C97406	hypothetical prote
214	3	8.8	34	2	S57282	phospholipase A2 (
215	3	8.8	34	2	A40298	dermaseptin - Sauv
216	3	8.8	34	2	JS0426	big gastrin - goat
217	3	8.8	34	2	I48887	cryptdin-4 - mouse
218	3	8.8	34	2	I32502	T-cell receptor de
219	3	8.8	34	2	H31461	T-cell receptor de
220	3	8.8	34	2	A19197	class II histocomp
221	3	8.8	34	2	D48147	troponin I (altern
222	3	8.8	34	2	A43564	neurogenic protein
223	3	8.8	34	2	H95047	hypothetical prote
224	3	8.8	34	2	D95189	hypothetical prote
225	3	8.8	34	2	C90973	hypothetical prote
226	3	8.8	34	2	F70242	hypothetical prote
227	3	8.8	34	2	B70252	hypothetical prote
228	3	8.8	34	2	F81919	hypothetical prote
229	3	8.8	34	2	H81883	hypothetical prote
230	3	8.8	34	2	F81044	hypothetical prote
231	3	8.8	34	2	F82163	hypothetical prote
232	3	8.8	34	2	E82100	hypothetical prote
233	3	8.8	34	2	B82449	hypothetical prote
234	3	8.8	34	2	S13662	cellulase (EC 3.2.
235	3	8.8	34	2	A60110	repetitive protein
236	3	8.8	34	2	S44828	F54F2.3 protein -
237	3	8.8	34	2	S40662	P-cadherin - mouse
238	3	8.8	34	2	F84079	hypothetical prote
239	3	8.8	34	2	H81600	hypothetical prote
240	3	8.8	34	2	H82820	hypothetical prote
241	3	8.8	34	2	C82819	hypothetical prote



242	3	8.8	34	2	C82764	hypothetical prote
243	3	8.8	34	2	B82679	hypothetical prote
244	3	8.8	34	2	G85820	unknown protein en
245	3	8.8	34	2	S12554	hydroxymethylgluta
246	3	8.8	35	2	E38601	Ig kappa chain V r
247	3	8.8	35	2	A05302	hemoglobin beta ch
248	3	8.8	35	2	A29663	histone H4 - starf
249	3	8.8	35	2	S27154	ribosomal protein
250	3	8.8	35	2	E48401	ribosomal protein
251	3	8.8	35	2	S13435	lectin III - furze
252	3	8.8	35	2	S74556	photosystem II psb
253	3	8.8	35	2	S18224	filamentous hemagg
254	3	8.8	35	2	S18226	opacity protein op
255	3	8.8	35	2	T07870	major latex protei
256	3	8.8	35	2	B33770	hypothetical prote
257	3	8.8	35	2	PS0439	potassium channel
258	3	8.8	35	2	I48925	homeobox protein -
259	3	8.8	35	2	F87622	hypothetical prote
260	3	8.8	35	2	C96619	protein T30E16.7 [
261	3	8.8	35	2	B84674	hypothetical prote
262	3	8.8	35	2	F84395	hypothetical prote
263	3	8.8	35	2	B82012	hypothetical prote
264	3	8.8	35	2	H81948	hypothetical prote
265	3	8.8	35	2	A82151	hypothetical prote
266	3	8.8	35	2	F82051	hypothetical prote
267	3	8.8	35	2	I64003	hypothetical prote
268	3	8.8	35	2	S58708	neutral phosphatas
269	3	8.8	35	2	F69827	hypothetical prote
270	3	8.8	35	2	C69977	hypothetical prote
271	3	8.8	35	2	S65772	early nodulin 40 -
272	3	8.8	35	2	G60529	hemocyanin M3' - c
273	3	8.8	35	2	A38107	mammalian toxin -
274	3	8.8	35	2	S49309	oncofetal protein
275	3	8.8	35	2	C81560	hypothetical prote
276	3	8.8	35	2	B85708	unknown protein en
277	3	8.8	36	2	H32502	T-cell receptor de
278	3	8.8	36	2	C32502	T-cell receptor de
279	3	8.8	36	2	S08552	ribosomal protein
280	3	8.8	36	2	S72299	ribosomal protein
281	3	8.8	36	2	B44400	myosin heavy chain
282	3	8.8	36	2	I46593	myosin - pig (frag
283	3	8.8	36	2	B31872	retinoic acid-bind
284	3	8.8	36	2	S35572	zona pellucida pro
285	3	8.8	36	2	B41481	virulence-associat
286	3	8.8	36	2	A38659	methanol dehydroge
287	3	8.8	36	2	C95218	conserved domain p
288	3	8.8	36	2	E84416	hypothetical prote
289	3	8.8	36	2	S17834	acetyl-CoA carboxy
290	3	8.8	36	2	E70220	hypothetical prote
291	3	8.8	36	2	E70238	hypothetical prote
292	3	8.8	36	2	F64604	hypothetical prote
293	3	8.8	36	2	G81853	hypothetical prote
294	3	8.8	36	2	S16552	hypothetical prote
295	3	8.8	36	2	G82281	hypothetical prote
296	3	8.8	36	2	A82163	hypothetical prote
297	3	8.8	36	2	C82111	hypothetical prote
298	3	8.8	36	2	A82092	hypothetical prote

299	3	8.8	36	2	B82093	hypothetical prote
300	3	8.8	36	2	A82437	hypothetical prote
301	3	8.8	36	2	A38729	pyruvate decarboxy
302	3	8.8	36	2	A69326	hypothetical prote
303	3	8.8	36	2	S67795	probable membrane
304	3	8.8	36	2	T22263	hypothetical prote
305	3	8.8	36	2	A57443	guanylate cyclase
306	3	8.8	36	2	D83682	hypothetical prote
307	3	8.8	36	2	A83870	hypothetical prote
308	3	8.8	36	2	F84074	hypothetical prote
309	3	8.8	36	2	A56634	neuropeptide F - A
310	3	8.8	36	2	S77071	probable plastoqui
311	3	8.8	36	2	AF1015	hypothetical prote
312	3	8.8	36	2	AI1841	hypothetical prote
313	3	8.8	37	1	S32792	iberiotoxin - east
314	3	8.8	37	1	HSWT93	histone H2A.3 - wh
315	3	8.8	37	2	S48656	fusicoccin recepto
316	3	8.8	37	2	S03570	trypsin (EC 3.4.21
317	3	8.8	37	2	S39367	proteinase omega -
318	3	8.8	37	2	S06217	transforming prote
319	3	8.8	37	2	S05037	insulinoma amyloid
320	3	8.8	37	2	A30607	Ig kappa chain V-I
321	3	8.8	37	2	PC1121	antifungal 25K pro
322	3	8.8	37	2	G01887	MEK kinase - human
323	3	8.8	37	2	S07517	gene 6.3 protein -
324	3	8.8	37	2	G70223	hypothetical prote
325	3	8.8	37	2	E70241	hypothetical prote
326	3	8.8	37	2	D83199	hypothetical prote
327	3	8.8	37	2	H82304	hypothetical prote
328	3	8.8	37	2	S21132	photosystem II cyt
329	3	8.8	37	2	F59103	hypothetical prote
330	3	8.8	37	2	T36662	small hypothetical
331	3	8.8	37	2	T11815	hypothetical prote
332	3	8.8	37	2	A57127	diuretic hormone 1
333	3	8.8	37	2	C32112	R15 gamma peptide
334	3	8.8	37	2	B48845	sterol regulatory
335	3	8.8	37	2	S68261	hypothetical prote
336	3	8.8	37	2	S49982	Tcell receptor alp
337	3	8.8	37	2	B39030	androgen-binding p
338	3	8.8	37	2	PN0550	metabotropic gluta
339	3	8.8	37	2	S70931	histone-like prote
340	3	8.8	37	2	F81403	hypothetical prote
341	3	8.8	38	1	R5EC36	ribosomal protein
342	3	8.8	38	2	C34047	stylar glycoprotei
343	3	8.8	38	2	T11763	acetyl-CoA carboxy
344	3	8.8	38	2	S39034	lipid transfer pro
345	3	8.8	38	2	A42974	natriuretic peptid
346	3	8.8	38	2	A49165	pituitary adenylat
347	3	8.8	38	2	A61070	pituitary adenylat
348	3	8.8	38	2	PS0129	H-2 class I histoc
349	3	8.8	38	2	S50764	ribosomal protein
350	3	8.8	38	2	E72247	ribosomal protein
351	3	8.8	38	2	H83113	50S ribosomal prot
352	3	8.8	38	2	AG0028	50S ribosomal prot
353	3	8.8	38	2	D91149	50S ribosomal subu
354	3	8.8	38	2	AF1008	50S ribosomal chai
355	3	8.8	38	2	PH1920	annexin-like 40K p

356	3	8.8	38	2	S72344	pileE protein - Nei
357	3	8.8	38	2	A60216	hyperglycemic horm
358	3	8.8	38	2	S65416	pyruvate synthase
359	3	8.8	38	2	B95069	hypothetical prote
360	3	8.8	38	2	A95139	hypothetical prote
361	3	8.8	38	2	H91111	hypothetical prote
362	3	8.8	38	2	D90631	hypothetical prote
363	3	8.8	38	2	E72306	hypothetical prote
364	3	8.8	38	2	E81873	hypothetical prote
365	3	8.8	38	2	T14885	hypothetical prote
366	3	8.8	38	2	A82478	hypothetical prote
367	3	8.8	38	2	E82463	hypothetical prote
368	3	8.8	38	2	A82450	hypothetical prote
369	3	8.8	38	2	D37842	hypothetical prote
370	3	8.8	38	2	B69492	hypothetical prote
371	3	8.8	38	2	S23173	photosystem I chai
372	3	8.8	38	2	T01992	hypothetical prote
373	3	8.8	38	2	S58601	hypothetical prote
374	3	8.8	38	2	T01741	hypothetical prote
375	3	8.8	38	2	B39888	synapsin I - bovin
376	3	8.8	38	2	B49012	orf 5' of megl - m
377	3	8.8	38	2	A83863	hypothetical prote
378	3	8.8	38	2	H81603	hypothetical prote
379	3	8.8	38	2	E82858	hypothetical prote
380	3	8.8	38	2	G71305	probable ribosomal
381	3	8.8	38	2	B97327	hypothetical prote
382	3	8.8	38	2	E86077	hypothetical prote
383	3	8.8	38	2	H85994	50S ribosomal subu
384	3	8.8	38	2	T08652	hypothetical prote
385	3	8.8	38	2	AB0747	hypothetical prote
386	3	8.8	38	2	AH0774	hypothetical prote
387	3	8.8	38	2	C97551	hypothetical prote
388	3	8.8	39	1	CTDFAS	corticotropin - sp
389	3	8.8	39	1	HWGH3Z	exendin-3 - Mexica
390	3	8.8	39	1	HWGH4G	exendin-4 - Gila m
391	3	8.8	39	2	B45946	gamma-glutamyltran
392	3	8.8	39	2	I55325	aspartate transami
393	3	8.8	39	2	S09645	hygromycin-B kinas
394	3	8.8	39	2	A01458	corticotropin - fi
395	3	8.8	39	2	PN0127	corticotropin - se
396	3	8.8	39	2	A61127	adrenocorticotropi
397	3	8.8	39	2	A01459	corticotropin - os
398	3	8.8	39	2	A01457	corticotropin - ra
399	3	8.8	39	2	C55995	prostaglandin E2 r
400	3	8.8	39	2	S07458	Ig kappa chain V r
401	3	8.8	39	2	PH0878	Ig kappa chain V r
402	3	8.8	39	2	S72459	ribosomal protein
403	3	8.8	39	2	PQ0011	tubulin beta chain
404	3	8.8	39	2	S63482	tubulin beta chain
405	3	8.8	39	2	A45793	actin - nematode (
406	3	8.8	39	2	AH2286	photosystem II pro
407	3	8.8	39	2	G64944	yebJ protein - Esc
408	3	8.8	39	2	A85795	hypothetical prote
409	3	8.8	39	2	S78008	fucosyltransferase
410	3	8.8	39	2	A48110	RNA recognition mo
411	3	8.8	39	2	H95146	hypothetical prote
412	3	8.8	39	2	D70239	hypothetical prote

413	3	8.8	39	2	C70254	hypothetical prote
414	3	8.8	39	2	G81899	hypothetical prote
415	3	8.8	39	2	B81912	hypothetical prote
416	3	8.8	39	2	B81954	very hypothetical
417	3	8.8	39	2	F82329	hypothetical prote
418	3	8.8	39	2	A43591	43K outer membrane
419	3	8.8	39	2	A44918	lactococcin G pept
420	3	8.8	39	2	S67938	hypothetical prote
421	3	8.8	39	2	S73118	photosystem II pro
422	3	8.8	39	2	PC4294	high mobility grou
423	3	8.8	39	2	T15158	hypothetical prote
424	3	8.8	39	2	I46466	luteinizing hormon
425	3	8.8	39	2	B40984	finger protein zfe
426	3	8.8	39	2	T03365	gene e2 protein -
427	3	8.8	39	2	F81587	hypothetical prote
428	3	8.8	39	2	E81540	hypothetical prote
429	3	8.8	39	2	T12905	hypothetical prote
430	3	8.8	39	2	AD0162	hypothetical prote
431	3	8.8	39	2	AE3109	hypothetical prote
432	3	8.8	40	1	SWFGS	sauvagine - Sauvag
433	3	8.8	40	2	B61320	plastocyanin - Aqu
434	3	8.8	40	2	S52343	hypothetical prote
435	3	8.8	40	2	S00264	creatine kinase (E
436	3	8.8	40	2	S34407	adenylate kinase (
437	3	8.8	40	2	PQ0202	endo-1,4-beta-xyla
438	3	8.8	40	2	S50021	trypsin-like prote
439	3	8.8	40	2	B60908	beta-lactamase (EC
440	3	8.8	40	2	B41440	protein disulfide-
441	3	8.8	40	2	A19940	antithrombin III -
442	3	8.8	40	2	B59005	thymosin beta - sc
443	3	8.8	40	2	A59005	thymosin beta - se
444	3	8.8	40	2	B31791	sarcotoxin ID - fl
445	3	8.8	40	2	S07969	T-cell receptor al
446	3	8.8	40	2	I50012	MHC class I protei
447	3	8.8	40	2	I50013	MHC class I protei
448	3	8.8	40	2	S61539	ribosomal protein
449	3	8.8	40	2	A60171	proteoglycan core
450	3	8.8	40	2	A60645	tubulin beta chain
451	3	8.8	40	2	A29184	vitellogenin - tur
452	3	8.8	40	2	S65907	conglutin gamma -
453	3	8.8	40	2	S08656	protein VI - human
454	3	8.8	40	2	A53708	indolepyruvate syn
455	3	8.8	40	2	T08107	nonenzymatic prote
456	3	8.8	40	2	S71917	hemoglobin, extrac
457	3	8.8	40	2	S58853	homeotic protein u
458	3	8.8	40	2	H95063	hypothetical prote
459	3	8.8	40	2	H91281	hypothetical prote
460	3	8.8	40	2	A87642	hypothetical prote
461	3	8.8	40	2	F87419	hypothetical prote
462	3	8.8	40	2	C32338	hypothetical 4K pr
463	3	8.8	40	2	C72398	hypothetical prote
464	3	8.8	40	2	S44935	hypothetical prote
465	3	8.8	40	2	A82203	hypothetical prote
466	3	8.8	40	2	G82484	hypothetical prote
467	3	8.8	40	2	A82382	hypothetical prote
468	3	8.8	40	2	I39944	regulatory extrace
469	3	8.8	40	2	F69677	phosphatase (RapK)

470	3	8.8	40	2	I41476	probable antigen 9
471	3	8.8	40	2	S27709	hypothetical prote
472	3	8.8	40	2	F45095	photosystem I ligh
473	3	8.8	40	2	T11811	hypothetical prote
474	3	8.8	40	2	T07472	hypothetical prote
475	3	8.8	40	2	T07516	hypothetical prote
476	3	8.8	40	2	T07523	hypothetical prote
477	3	8.8	40	2	T07560	hypothetical prote
478	3	8.8	40	2	T48629	hypothetical prote
479	3	8.8	40	2	S53001	mitotic-specific c
480	3	8.8	40	2	T03831	hypothetical prote
481	3	8.8	40	2	S71295	deoxyguanosine kin
482	3	8.8	40	2	S56768	capsid protein - L
483	3	8.8	40	2	T07206	hypothetical prote
484	3	8.8	40	2	H81592	hypothetical prote
485	3	8.8	40	2	H81520	hypothetical prote
486	3	8.8	40	2	F81511	hypothetical prote
487	3	8.8	40	2	G82620	hypothetical prote
488	3	8.8	40	2	A82590	hypothetical prote
489	3	8.8	40	2	A86123	hypothetical prote
490	3	8.8	40	2	B97413	hypothetical prote
491	2	5.9	28	1	LFSEW	trp operon leader
492	2	5.9	28	1	LFEBLT	leu operon leader
493	2	5.9	28	1	LFECL	leu operon leader
494	2	5.9	28	1	G9BPSV	gene 9 protein - s
495	2	5.9	28	2	S41774	ubiquinol-cytochro
496	2	5.9	28	2	S71598	cytochrome P450 HP
497	2	5.9	28	2	S04341	cytochrome P450 PB
498	2	5.9	28	2	PX0033	cytochrome P450 te
499	2	5.9	28	2	S66436	allophycocyanin al
500	2	5.9	28	2	S47624	D-aspartate oxidas
501	2	5.9	28	2	T14210	NADH2 dehydrogenas
502	2	5.9	28	2	T14213	NADH2 dehydrogenas
503	2	5.9	28	2	T12301	NADH2 dehydrogenas
504	2	5.9	28	2	PC1162	cytochrome-c oxida
505	2	5.9	28	2	S21278	glutathione transf
506	2	5.9	28	2	C33948	glutathione transf
507	2	5.9	28	2	A34244	hexokinase (EC 2.7
508	2	5.9	28	2	D38578	protein kinase 4 (
509	2	5.9	28	2	B39116	epidermal growth f
510	2	5.9	28	2	A31859	deoxycytidine kina
511	2	5.9	28	2	B54257	deoxynucleoside ki
512	2	5.9	28	2	I55596	lysosomal acid lip
513	2	5.9	28	2	B35948	phospholipase A2 (
514	2	5.9	28	2	C35948	phospholipase A2 (
515	2	5.9	28	2	A35115	hypothetical prote
516	2	5.9	28	2	A61281	lysozyme homolog A
517	2	5.9	28	2	A61529	chymotrypsin (EC 3
518	2	5.9	28	2	A60291	24K proteinase (EC
519	2	5.9	28	2	S08186	proteasome beta ch
520	2	5.9	28	2	S55729	orotidine-5'-monop
521	2	5.9	28	2	I40034	trpE protein - Bac
522	2	5.9	28	2	A32643	deoxyribodipyrimid
523	2	5.9	28	2	S77854	glutamate-tRNA lig
524	2	5.9	28	2	JX0059	serine proteinase
525	2	5.9	28	2	S07156	trypsin inhibitor
526	2	5.9	28	2	JX0058	trypsin inhibitor

527	2	5.9	28	2	B45041	trypsin inhibitor
528	2	5.9	28	2	S20393	trypsin inhibitor
529	2	5.9	28	2	A25802	2S seed storage pr
530	2	5.9	28	2	T47196	RAS protein [impor
531	2	5.9	28	2	A61322	somatostatin-28 -
532	2	5.9	28	2	B60583	glycoprotein hormo
533	2	5.9	28	2	A38232	vasoactive intesti
534	2	5.9	28	2	A60303	vasoactive intesti
535	2	5.9	28	2	JT0412	bombyxin-IV chain
536	2	5.9	28	2	A56366	intestinal trefoil
537	2	5.9	28	2	C44180	alpha-neurotoxin-l
538	2	5.9	28	2	C39327	long neurotoxin -
539	2	5.9	28	2	I32529	Ig lambda chain V
540	2	5.9	28	2	PC1001	Ig light chain V r
541	2	5.9	28	2	B47719	T-cell receptor al
542	2	5.9	28	2	D47719	T-cell receptor al
543	2	5.9	28	2	S58389	T-cell receptor be
544	2	5.9	28	2	PH0250	T-cell receptor Vb
545	2	5.9	28	2	PH0247	T-cell receptor Vb
546	2	5.9	28	2	A49829	T-cell receptor va
547	2	5.9	28	2	D49829	T-cell receptor va
548	2	5.9	28	2	PH1908	T-cell receptor al
549	2	5.9	28	2	D41912	T-cell receptor be
550	2	5.9	28	2	G47719	house-dust-mite-re
551	2	5.9	28	2	E49533	T-cell receptor be
552	2	5.9	28	2	I46921	gene Bota protein
553	2	5.9	28	2	S11618	ribosomal protein
554	2	5.9	28	2	S51060	ribosomal protein
555	2	5.9	28	2	S51067	ribosomal protein
556	2	5.9	28	2	S72460	ribosomal protein
557	2	5.9	28	2	S08569	ribosomal protein
558	2	5.9	28	2	S10052	ribosomal protein
559	2	5.9	28	2	S55442	beta A2 crystallin
560	2	5.9	28	2	A45626	beta 2-tubulin - n
561	2	5.9	28	2	S21231	calcium-binding pr
562	2	5.9	28	2	A23691	apolipoprotein C-I
563	2	5.9	28	2	A05296	fibrinogen alpha c
564	2	5.9	28	2	A61113	cellular retinol-b
565	2	5.9	28	2	B35577	cell adhesion rece
566	2	5.9	28	2	I48349	fibronectin - mous
567	2	5.9	28	2	A61233	retinol-binding pr
568	2	5.9	28	2	I45911	dnaK-type molecula
569	2	5.9	28	2	PQ0263	dnaK-type molecula
570	2	5.9	28	2	A03356	omega-gliadin - ei
571	2	5.9	28	2	A60359	pollen allergen DG
572	2	5.9	28	2	A60752	outer membrane pro
573	2	5.9	28	2	PQ0691	photosystem I 5.6K
574	2	5.9	28	2	G32351	34K class B flagel
575	2	5.9	28	2	S47614	zinc finger protei
576	2	5.9	28	2	S49924	stp protein (Baker
577	2	5.9	28	2	B39227	calcium channel pr
578	2	5.9	28	2	F54346	pyruvate synthase
579	2	5.9	28	2	A36153	major allergen Ole
580	2	5.9	28	2	B54127	dolichyl-diphospho
581	2	5.9	28	2	S56746	alpha-synuclein, N
582	2	5.9	28	2	I48178	orphan receptor -
583	2	5.9	28	2	PC4429	peroxisome prolife

584	2	5.9	28	2	PC4430	peroxisome prolife
585	2	5.9	28	2	S29135	aminopyrine N-deme
586	2	5.9	28	2	S29136	aminopyrine N-deme
587	2	5.9	28	2	PN0625	homeobox JRX prote
588	2	5.9	28	2	B56779	tetM 5'-region lea
589	2	5.9	28	2	JU0297	fruR-shl operon le
590	2	5.9	28	2	G90638	leu operon leader
591	2	5.9	28	2	C90639	fruR leader peptid
592	2	5.9	28	2	B47310	MHVS28AA - murine
593	2	5.9	28	2	E64656	hypothetical prote
594	2	5.9	28	2	B64669	hypothetical prote
595	2	5.9	28	2	S15235	hypothetical prote
596	2	5.9	28	2	C56262	uvrB 3'-region hyp
597	2	5.9	28	2	E81239	hypothetical prote
598	2	5.9	28	2	I60364	phosphorybosylpyro
599	2	5.9	28	2	B39191	hypothetical prote
600	2	5.9	28	2	T17391	hypothetical prote
601	2	5.9	28	2	A56499	brevicin-27 - Lact
602	2	5.9	28	2	A41476	probable antigen 1
603	2	5.9	28	2	S16228	aryl acylamidase -
604	2	5.9	28	2	T37143	hypothetical prote
605	2	5.9	28	2	PS0106	2-phosphinomethylm
606	2	5.9	28	2	G69384	conserved hypothet
607	2	5.9	28	2	A69259	hypothetical prote
608	2	5.9	28	2	T06925	hypothetical prote
609	2	5.9	28	2	S38524	rRNA N-glycosidase
610	2	5.9	28	2	S21742	3-oxoacyl-[acyl-ca
611	2	5.9	28	2	PQ0800	calmodulin antagon
612	2	5.9	28	2	T06340	ribosomal protein
613	2	5.9	28	2	T07599	hypothetical prote
614	2	5.9	28	2	PH0220	peroxidase (EC 1.1
615	2	5.9	28	2	JQ0272	hypothetical 3K pr
616	2	5.9	28	2	S46250	fatty-acid-binding
617	2	5.9	28	2	A44923	carboxypeptidase 3
618	2	5.9	28	2	S64701	hypothetical prote
619	2	5.9	28	2	T38041	similarity to yeas
620	2	5.9	28	2	A60698	trichocyst protein
621	2	5.9	28	2	A27261	proteinase inhibit
622	2	5.9	28	2	A61417	bdellin B-3 - medi
623	2	5.9	28	2	S06668	toxin-like protein
624	2	5.9	28	2	S07826	venom protein - Am
625	2	5.9	28	2	C34923	omega-agatoxin IIA
626	2	5.9	28	2	A44877	cell surface prote
627	2	5.9	28	2	JW0019	mast cell degranul
628	2	5.9	28	2	A61273	interleukin-1 - st
629	2	5.9	28	2	S68643	nicotinic acetylch
630	2	5.9	28	2	PC2162	angiotensin II rec
631	2	5.9	28	2	I54183	cell adhesion regu
632	2	5.9	28	2	S54338	cytochrome P450 CY
633	2	5.9	28	2	I52627	erythrocyte chemok
634	2	5.9	28	2	JQ1035	hypothetical 3.2K
635	2	5.9	28	2	PH1335	Ig heavy chain DJ
636	2	5.9	28	2	S37683	protein IEF SSP 91
637	2	5.9	28	2	S37686	protein IEF SSP 92
638	2	5.9	28	2	PH1911	T-cell receptor al
639	2	5.9	28	2	I39288	ZF3 domain - human
640	2	5.9	28	2	PL0005	pepsin A (EC 3.4.2

641	2	5.9	28	2	A60692	proline-rich prote
642	2	5.9	28	2	PC2239	heat shock protein
643	2	5.9	28	2	PT0366	T-cell receptor be
644	2	5.9	28	2	I58115	cystic fibrosis tr
645	2	5.9	28	2	A46690	sialic acid-specif
646	2	5.9	28	2	C83797	hypothetical prote
647	2	5.9	28	2	C83969	hypothetical prote
648	2	5.9	28	2	S51593	myrB protein - Mic
649	2	5.9	28	2	C85490	fruR leader peptid
650	2	5.9	28	2	C97078	hypothetical prote
651	2	5.9	28	2	F97000	hypothetical prote
652	2	5.9	28	2	G85489	leu operon leader
653	2	5.9	28	2	AB1093	hypothetical prote
654	2	5.9	28	2	T06490	probable ribulose-
655	2	5.9	28	2	S73563	H+-transporting tw
656	2	5.9	28	2	AG0516	leu operon leader
657	2	5.9	28	4	I68614	frame shifted FMR1
658	2	5.9	28	4	JN0014	GABA(A) receptor a
659	2	5.9	29	1	TIPU	trypsin inhibitor
660	2	5.9	29	1	TIPU3	trypsin inhibitor
661	2	5.9	29	1	TIPU2B	trypsin inhibitor
662	2	5.9	29	1	GCOPV	glucagon - North A
663	2	5.9	29	1	GCDK	glucagon - duck
664	2	5.9	29	1	A61583	glucagon - ostrich
665	2	5.9	29	1	GCFLE	glucagon - Europea
666	2	5.9	29	1	GCDF	glucagon - smaller
667	2	5.9	29	1	GCEN	glucagon - elephan
668	2	5.9	29	1	GCTTS	glucagon - slider
669	2	5.9	29	1	TNLJBR	trans-activating t
670	2	5.9	29	1	Q1BP57	gene 1.5 protein -
671	2	5.9	29	2	A60558	cytochrome P450 HL
672	2	5.9	29	2	T17079	NADH2 dehydrogenas
673	2	5.9	29	2	T17076	NADH2 dehydrogenas
674	2	5.9	29	2	A48427	flavohemoglobin hm
675	2	5.9	29	2	A54234	cytochrome-c oxida
676	2	5.9	29	2	S08201	peroxidase (EC 1.1
677	2	5.9	29	2	A26208	acetyl-CoA C-acety
678	2	5.9	29	2	A22018	phosphotransferase
679	2	5.9	29	2	S46211	kallikrein rK8 (pK
680	2	5.9	29	2	S28174	heat-shock protein
681	2	5.9	29	2	A32414	bothrolysin (EC 3.
682	2	5.9	29	2	S17432	H+-transporting tw
683	2	5.9	29	2	S02578	H+-transporting tw
684	2	5.9	29	2	S23122	peptidylprolyl iso
685	2	5.9	29	2	JU0211	squash-type trypsi
686	2	5.9	29	2	T03653	phospholipid trans
687	2	5.9	29	2	C24536	alpha-amylase/tryp
688	2	5.9	29	2	C25310	alpha-amylase/tryp
689	2	5.9	29	2	D55998	brevinin-2Ed - edi
690	2	5.9	29	2	D53578	brevinin-2Ee - edi
691	2	5.9	29	2	A91740	glucagon - turkey
692	2	5.9	29	2	A91741	glucagon - rabbit
693	2	5.9	29	2	A91742	glucagon - Arabian
694	2	5.9	29	2	S07211	glucagon - marbled
695	2	5.9	29	2	A61135	glucagon - bigeye
696	2	5.9	29	2	C39258	glucagon - common
697	2	5.9	29	2	C60840	glucagon I - Europ



698	2	5.9	29	2	S39018	glucagon - bowfin
699	2	5.9	29	2	A39462	cholestinin - do
700	2	5.9	29	2	A60791	toxin II.9 - scorp
701	2	5.9	29	2	JH0699	omega-conotoxin MV
702	2	5.9	29	2	A58537	omega-conotoxin MV
703	2	5.9	29	2	I52628	low affinity nerve
704	2	5.9	29	2	C61233	conceptus protein
705	2	5.9	29	2	S10061	Ig heavy chain (cl
706	2	5.9	29	2	PH1328	Ig heavy chain DJ
707	2	5.9	29	2	PH0239	T-cell receptor Vb
708	2	5.9	29	2	PH0251	T-cell receptor Vb
709	2	5.9	29	2	PH0254	T-cell receptor Vb
710	2	5.9	29	2	PH0233	T-cell receptor Vb
711	2	5.9	29	2	E31485	Ig heavy chain V r
712	2	5.9	29	2	H31485	Ig kappa chain V r
713	2	5.9	29	2	G31461	T-cell receptor de
714	2	5.9	29	2	C47719	T-cell receptor al
715	2	5.9	29	2	E47719	house-dust-mite-re
716	2	5.9	29	2	PS0134	H-2 class I histoc
717	2	5.9	29	2	PS0132	H-2 class I histoc
718	2	5.9	29	2	D32533	class II histocomp
719	2	5.9	29	2	I37534	gene HLA-DRB prote
720	2	5.9	29	2	I37535	gene HLA-DRB prote
721	2	5.9	29	2	I37536	MHC class II histo
722	2	5.9	29	2	I37301	MHC class II histo
723	2	5.9	29	2	I37303	HLA-DR beta - huma
724	2	5.9	29	2	I37306	HLA-DR beta - huma
725	2	5.9	29	2	I50214	protein-tyrosine-p
726	2	5.9	29	2	S07771	histone H2B.2, spe
727	2	5.9	29	2	T04412	histone H3 - barle
728	2	5.9	29	2	S51070	ribosomal protein
729	2	5.9	29	2	S08555	ribosomal protein
730	2	5.9	29	2	PC4231	ribosomal protein
731	2	5.9	29	2	S10050	ribosomal protein
732	2	5.9	29	2	S10049	ribosomal protein
733	2	5.9	29	2	S26229	ribosomal protein
734	2	5.9	29	2	A27561	Meth A tumor-speci
735	2	5.9	29	2	S10725	calmodulin-binding
736	2	5.9	29	2	E33208	calreticulin, uter
737	2	5.9	29	2	C33208	calreticulin, slow
738	2	5.9	29	2	D33208	calreticulin, brai
739	2	5.9	29	2	A45474	thrombospondin 2 -
740	2	5.9	29	2	G39690	neural cell adhesi
741	2	5.9	29	2	A61166	endometrial proges
742	2	5.9	29	2	I52402	alpha-fetoprotein
743	2	5.9	29	2	S00564	enamel protein - r
744	2	5.9	29	2	S57232	homeotic protein s
745	2	5.9	29	2	S06854	chorion class B pr
746	2	5.9	29	2	A43038	auxin-binding prot
747	2	5.9	29	2	T12082	proline-rich prote
748	2	5.9	29	2	S70328	gamma35 secalin -
749	2	5.9	29	2	S29208	avenin gamma-3 - o
750	2	5.9	29	2	S07055	photosystem I prot
751	2	5.9	29	2	S05032	photosystem II pro
752	2	5.9	29	2	S08088	gene VII protein -
753	2	5.9	29	2	F42075	finger protein (cl
754	2	5.9	29	2	T51116	probable precorrin

755	2	5.9	29	2	A53145	high conductance c
756	2	5.9	29	2	A35121	hypothetical prote
757	2	5.9	29	2	S03277	photosystem II 5K
758	2	5.9	29	2	S63509	glycine reductase
759	2	5.9	29	2	A55891	delta-conotoxin Gm
760	2	5.9	29	2	S32730	homeotic protein -
761	2	5.9	29	2	S57225	labial protein (cl
762	2	5.9	29	2	S32732	homeotic protein -
763	2	5.9	29	2	S32734	homeotic protein -
764	2	5.9	29	2	S32733	homeotic protein -
765	2	5.9	29	2	G90719	hypothetical prote
766	2	5.9	29	2	S07513	gene 5.1 protein -
767	2	5.9	29	2	S14040	hypothetical prote
768	2	5.9	29	2	E64586	hypothetical prote
769	2	5.9	29	2	B64607	hypothetical prote
770	2	5.9	29	2	G64674	hypothetical prote
771	2	5.9	29	2	G83440	KdpF protein PA163
772	2	5.9	29	2	A49288	alcohol dehydrogen
773	2	5.9	29	2	A81078	hypothetical prote
774	2	5.9	29	2	B81006	hypothetical prote
775	2	5.9	29	2	T48910	KdpF protein [vali
776	2	5.9	29	2	A35445	repY protein - Esc
777	2	5.9	29	2	S19943	aadB protein - Kle
778	2	5.9	29	2	A49914	S-layer protein va
779	2	5.9	29	2	E64036	hypothetical prote
780	2	5.9	29	2	B48363	2-hydroxyglutaryl-
781	2	5.9	29	2	C40638	orf 3' of cycI - R
782	2	5.9	29	2	S05224	photosystem I 4.8K
783	2	5.9	29	2	B56817	photosystem I chai
784	2	5.9	29	2	S74572	hypothetical prote
785	2	5.9	29	2	C60743	putrescine caramo
786	2	5.9	29	2	S67989	HA-19/HA-52 protei
787	2	5.9	29	2	S14099	12-alpha-hydroxyst
788	2	5.9	29	2	S77569	plantaricin SA6 -
789	2	5.9	29	2	S21222	48K protein - Euba
790	2	5.9	29	2	S03947	hydrogen dehydroge
791	2	5.9	29	2	T34643	hypothetical prote
792	2	5.9	29	2	T37120	hypothetical prote
793	2	5.9	29	2	T36654	probable small mem
794	2	5.9	29	2	B43937	endo-1,4-beta-xyla
795	2	5.9	29	2	S09556	hypothetical prote
796	2	5.9	29	2	T06904	hypothetical prote
797	2	5.9	29	2	S73197	hypothetical prote
798	2	5.9	29	2	S78326	conserved hypothet
799	2	5.9	29	2	S78310	hypothetical prote
800	2	5.9	29	2	S78360	hypothetical prote
801	2	5.9	29	2	S01572	hypothetical prote
802	2	5.9	29	2	T07450	hypothetical prote
803	2	5.9	29	2	S01448	hypothetical prote
804	2	5.9	29	2	S38525	rRNA N-glycosidase
805	2	5.9	29	2	T52557	translation elonga
806	2	5.9	29	2	PQ0862	allantoinase (EC 3
807	2	5.9	29	2	PQ0486	globulin 2a - taro
808	2	5.9	29	2	S02200	prolamin alpha-1 -
809	2	5.9	29	2	A60683	malate dehydrogena
810	2	5.9	29	2	JQ0212	hypothetical 3K pr
811	2	5.9	29	2	S58541	hypothetical prote

812	2	5.9	29	2	PC2035	alanine transamina
813	2	5.9	29	2	S78714	protein YDR524w-a
814	2	5.9	29	2	B21112	variant surface gl
815	2	5.9	29	2	C60110	repetitive protein
816	2	5.9	29	2	D24802	cuticle protein 36
817	2	5.9	29	2	A56591	E75 steroid recept
818	2	5.9	29	2	A61613	ceratotoxin A - Me
819	2	5.9	29	2	B61613	ceratotoxin B - Me
820	2	5.9	29	2	PH1230	lectin - namazu (f
821	2	5.9	29	2	A32860	biotin-binding pro
822	2	5.9	29	2	I50382	c-mil protein - ch
823	2	5.9	29	2	I50695	non-collagenous al
824	2	5.9	29	2	B54197	70k thyroid autoan
825	2	5.9	29	2	A35891	carcinoembryonic a
826	2	5.9	29	2	I77372	CD44SP - human
827	2	5.9	29	2	S54340	diazepam binding i
828	2	5.9	29	2	A41683	hyaluronate recept
829	2	5.9	29	2	C54037	splicing regulator
830	2	5.9	29	2	S35924	T-cell receptor ga
831	2	5.9	29	2	C61384	trachael mucin gly
832	2	5.9	29	2	A60604	glutathione peroxi
833	2	5.9	29	2	S57204	oviduct-specific s
834	2	5.9	29	2	I47025	antigen WC1 [impor
835	2	5.9	29	2	A49410	t-complex polypept
836	2	5.9	29	2	PS0125	H-2 class I histoc
837	2	5.9	29	2	S46929	tegl69 protein - m
838	2	5.9	29	2	S38749	vimentin homolog -
839	2	5.9	29	2	S42764	Ca2+/calmodulin-de
840	2	5.9	29	2	A49708	synaptosomal-assoc
841	2	5.9	29	2	H83777	hypothetical prote
842	2	5.9	29	2	C83833	hypothetical prote
843	2	5.9	29	2	F83870	hypothetical prote
844	2	5.9	29	2	B84144	hypothetical prote
845	2	5.9	29	2	PC4421	multactivase (EC 3
846	2	5.9	29	2	B85840	hypothetical prote
847	2	5.9	29	2	C85840	hypothetical prote
848	2	5.9	29	2	G86058	hypothetical prote
849	2	5.9	29	2	E89904	hypothetical prote
850	2	5.9	29	2	H89949	hypothetical prote
851	2	5.9	29	2	A59278	neurotoxin BmK A3-
852	2	5.9	29	2	S17496	inorganic diphosph
853	2	5.9	29	2	PQ0782	NADH2 dehydrogenas
854	2	5.9	29	2	S34762	L-serine ammonia-l
855	2	5.9	29	2	AB0717	hypothetical prote
856	2	5.9	29	2	AC0717	hypothetical prote
857	2	5.9	29	2	AH2338	PetN protein [impo
858	2	5.9	29	4	I58970	hypothetical prote
859	2	5.9	30	1	AIBSAF	thermophilic amino
860	2	5.9	30	1	TIPU1W	trypsin inhibitor
861	2	5.9	30	1	OEON2K	beta-endorphin II
862	2	5.9	30	1	IRTRC3	protamine CIII, ma
863	2	5.9	30	1	IRTRC2	protamine 1a - rai
864	2	5.9	30	1	IRTR78	protamine CIII, mi
865	2	5.9	30	1	IRTR4	protamine pTP4 - r
866	2	5.9	30	1	CLHRY2	protamine YII - Pa
867	2	5.9	30	1	CLHR2A	protamine YII - At
868	2	5.9	30	1	SNUMP	sillucin - Rhizomu

869	2	5.9	30	2	I57689	ubiquinol-cytochro
870	2	5.9	30	2	I52254	gene CYP11B2 prote
871	2	5.9	30	2	B56859	fatty acid omega-h
872	2	5.9	30	2	A27375	photosystem I iron
873	2	5.9	30	2	S11131	NADH2 dehydrogenas
874	2	5.9	30	2	S14214	NADH2 dehydrogenas
875	2	5.9	30	2	S08202	peroxidase (EC 1.1
876	2	5.9	30	2	S08204	peroxidase (EC 1.1
877	2	5.9	30	2	S08203	peroxidase (EC 1.1
878	2	5.9	30	2	A39089	hydrogenase (EC 1.
879	2	5.9	30	2	I38066	nitric-oxide synth
880	2	5.9	30	2	I39799	CAT-66 - Bacillus
881	2	5.9	30	2	A18780	dimethylallyltrans
882	2	5.9	30	2	S03283	methionine adenosy
883	2	5.9	30	2	S71865	glutathione transf
884	2	5.9	30	2	B27103	aspartate transami
885	2	5.9	30	2	A27103	aspartate transami
886	2	5.9	30	2	I55427	aspartate transami
887	2	5.9	30	2	A49955	protein-tyrosine k
888	2	5.9	30	2	S68639	nigroxin A - black
889	2	5.9	30	2	S68640	nigroxin B - black
890	2	5.9	30	2	A05004	pancreatic ribonuc
891	2	5.9	30	2	D57001	endo-1,4-beta-xyla
892	2	5.9	30	2	A43937	endo-1,4-beta-xyla
893	2	5.9	30	2	PC2361	alpha-glucosidase
894	2	5.9	30	2	PX0073	epoxide hydrolase
895	2	5.9	30	2	B60291	30K serine protein
896	2	5.9	30	2	A27634	major fecal allerg
897	2	5.9	30	2	B27634	major fecal allerg
898	2	5.9	30	2	I77411	renin-2 - mouse (f
899	2	5.9	30	2	PC2328	proteasome endopep
900	2	5.9	30	2	A34486	inorganic diphosph
901	2	5.9	30	2	S21816	H+-exporting ATPas
902	2	5.9	30	2	S21814	H+-exporting ATPas
903	2	5.9	30	2	S74121	fructose-bisphosph
904	2	5.9	30	2	S25666	phosphopyruvate hy
905	2	5.9	30	2	S69600	peptidylprolyl iso
906	2	5.9	30	2	A60517	alpha-1-antitrypsi
907	2	5.9	30	2	S24979	proteinase inhibit
908	2	5.9	30	2	JX0057	trypsin inhibitor
909	2	5.9	30	2	JS0579	squash-type trypsi
910	2	5.9	30	2	JQ1958	trypsin inhibitor
911	2	5.9	30	2	PC1113	proteinase inhibit
912	2	5.9	30	2	C42842	antifungal 2S stor
913	2	5.9	30	2	S70341	napin large chain
914	2	5.9	30	2	S70343	napin large chain
915	2	5.9	30	2	A33308	thrombomodulin - r
916	2	5.9	30	2	S01657	atrial natriuretic
917	2	5.9	30	2	A61130	somatotropin - Ame
918	2	5.9	30	2	S44473	glucagon-like pept
919	2	5.9	30	2	A59076	defensin alpha-1 -
920	2	5.9	30	2	B59076	defensin alpha-2 -
921	2	5.9	30	2	C59076	defensin alpha-3 -
922	2	5.9	30	2	B60791	toxin II.6 - scorp
923	2	5.9	30	2	A31187	neurotoxin II.22.5
924	2	5.9	30	2	I68109	interferon alpha-W
925	2	5.9	30	2	C49533	T-cell receptor al

926	2	5.9	30	2	S20778	Ig heavy chain V r
927	2	5.9	30	2	PL0092	Ig heavy chain V r
928	2	5.9	30	2	PH0245	T-cell receptor Vb
929	2	5.9	30	2	PH0228	T-cell receptor Vb
930	2	5.9	30	2	PH0252	T-cell receptor Vb
931	2	5.9	30	2	PH0882	Ig kappa chain V r
932	2	5.9	30	2	E31461	T-cell receptor de
933	2	5.9	30	2	PH0235	T-cell receptor Vb
934	2	5.9	30	2	A49533	T-cell receptor al
935	2	5.9	30	2	C27579	T-cell receptor be
936	2	5.9	30	2	I37626	Fc gamma (IgG) rec
937	2	5.9	30	2	PS0121	H-2 class I histoc
938	2	5.9	30	2	S74192	crotoxin inhibitor
939	2	5.9	30	2	A05253	hemoglobin epsilon
940	2	5.9	30	2	A21680	hemoglobin epsilon
941	2	5.9	30	2	A05254	hemoglobin epsilon
942	2	5.9	30	2	S68618	histone H2B - sea
943	2	5.9	30	2	PD0014	cAMP response elem
944	2	5.9	30	2	PN0651	restriction endonu
945	2	5.9	30	2	S11613	ribosomal protein
946	2	5.9	30	2	A60511	gamma-crystallin -
947	2	5.9	30	2	I49412	gamma-crystallin-3
948	2	5.9	30	2	S12965	gamma-crystallin -
949	2	5.9	30	2	S69269	ezrin homolog - bo
950	2	5.9	30	2	A61189	tubulin beta chain
951	2	5.9	30	2	I52806	Duchenne muscular
952	2	5.9	30	2	S21153	calcium-binding pr
953	2	5.9	30	2	A26188	lipocortin I - pig
954	2	5.9	30	2	A56790	annexin, isoform P
955	2	5.9	30	2	A34622	fibrinogen beta ch
956	2	5.9	30	2	A03148	retinol-binding pr
957	2	5.9	30	2	A48299	taurine transporte
958	2	5.9	30	2	B61511	serum albumin, mil
959	2	5.9	30	2	B39819	neutrophil chemota
960	2	5.9	30	2	A38933	vitronectin - bovi
961	2	5.9	30	2	S57234	fushi tarazu segme
962	2	5.9	30	2	S69124	rRNA N-glycosidase
963	2	5.9	30	2	S69125	rRNA N-glycosidase
964	2	5.9	30	2	S07065	rRNA N-glycosidase
965	2	5.9	30	2	A31836	17K antigen - Rick
966	2	5.9	30	2	PQ0669	photosystem I 17.5
967	2	5.9	30	2	E45095	photosystem I ligh
968	2	5.9	30	2	B45095	photosystem I ligh
969	2	5.9	30	2	B24987	regulatory protein
970	2	5.9	30	2	S30757	genome polyprotein
971	2	5.9	30	2	S30760	genome polyprotein
972	2	5.9	30	2	S30759	genome polyprotein
973	2	5.9	30	2	B44314	intracisternal A p
974	2	5.9	30	2	S13753	replication initia
975	2	5.9	30	2	S26175	tail tubular prote
976	2	5.9	30	2	S69352	N-methylhydantoin
977	2	5.9	30	2	S68312	glucuronosyltransf
978	2	5.9	30	2	PH1228	D-aminoacylase (EC
979	2	5.9	30	2	S42364	aromatic-amino-aci
980	2	5.9	30	2	S05223	photosystem I 6.5K
981	2	5.9	30	2	S28991	antifungal protein
982	2	5.9	30	2	PC2307	X-Pro aminopeptida

983	2	5.9	30	2	PQ0484	globulin 1b - taro
984	2	5.9	30	2	C43591	51K outer membrane
985	2	5.9	30	2	B43591	45K outer membrane
986	2	5.9	30	2	S06411	killer plasmid 28K
987	2	5.9	30	2	B49292	GDP dissociation i
988	2	5.9	30	2	A60914	pheromone-binding
989	2	5.9	30	2	PS0437	potassium channel
990	2	5.9	30	2	PS0438	potassium channel
991	2	5.9	30	2	A47607	immunogenic protei
992	2	5.9	30	2	S02088	blood group Rh-rel
993	2	5.9	30	2	S29138	aniline monooxygen
994	2	5.9	30	2	S57227	proboscipedia prot
995	2	5.9	30	2	H95008	hypothetical prote
996	2	5.9	30	2	C95030	hypothetical prote
997	2	5.9	30	2	G95031	hypothetical prote
998	2	5.9	30	2	E95079	hypothetical prote
999	2	5.9	30	2	F95118	hypothetical prote
1000	2	5.9	30	2	E95145	hypothetical prote

# ALIGNMENTS

## RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 14.7%; Score 5; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28

|||||

Db 26 LRKKL 30

## RESULT 2

B97032

transcription regulator, AcrR family [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 14.7%; Score 5; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5  
    ||||  
Db 30 SVSEI 34

## RESULT 3

E95098

hypothetical protein SP0853 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:  
A;Gene: SP0853

Query Match 14.7%; Score 5; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30  
|||||  
Db 30 KKLQD 34

RESULT 4

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity  
homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 11.8%; Score 4; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
|||||  
Db 15 LRKK 18

RESULT 5

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;  
Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.

J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of  
mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline  
quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary



A;Molecule type: DNA  
A;Residues: 1-29 <MOR>  
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590  
C;Genetics:  
A;Gene: pqqD  
C;Superfamily: pyrroloquinoline quinone precursor pqqA  
C;Keywords: quinoprotein  
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>  
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5  
|||  
Db 8 VSEI 11

RESULT 6

S01614  
dystrophin - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C;Accession: S01614  
R;Nudel, U.; Robzyk, K.; Yaffe, D.  
Nature 331, 635-638, 1988  
A;Title: Expression of the putative Duchenne muscular dystrophy gene in differentiated myogenic cell cultures and in the brain.  
A;Reference number: S01614; MUID:88122671; PMID:3340214  
A;Accession: S01614  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-29 <NUD>  
A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214  
C;Genetics:  
A;Map position: X  
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology; WW repeat homology  
C;Keywords: actin binding; cytoskeleton

Query Match 11.8%; Score 4; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30  
|||  
Db 12 KLQD 15

RESULT 7

I78537  
copper transporting P-type ATPase - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C;Accession: I78537  
R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 11.8%; Score 4; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6  
|||  
Db 14 SEIQ 17

#### RESULT 8

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10,'XXP',14-15,'X',17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 11.8%; Score 4; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
|||  
Db 4 LRKK 7

#### RESULT 9

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.  
 Eur. J. Biochem. 233, 800-808, 1995  
 A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate  
 dehydrogenase genes from the thermophilic archaeon *Sulfolobus solfataricus*  
 overlap by 8-bp: isolation, sequencing of the genes and expression in  
*Escherichia coli*.  
 A;Reference number: S63528; MUID:96085144; PMID:8521845  
 A;Accession: S63531  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-30 <JON>  
 A;Cross-references: EMBL:X80178

Query Match 11.8%; Score 4; DB 2; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26  
 ||||  
 Db 11 WLRK 14

# RESULT 10

S44471  
 glucagon G1 - North American paddlefish (*Polyodon spathula*)  
 C;Species: *Polyodon spathula*  
 C;Date: 18-Sep-1997 #sequence\_revision 18-Sep-1997 #text\_change 07-May-1999  
 C;Accession: S44471  
 R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.  
 Biochem. J. 300, 339-345, 1994  
 A;Title: Characterization of insulins and proglucagon-derived peptides from a  
 phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).  
 A;Reference number: S44467; MUID:94271144; PMID:8002937  
 A;Accession: S44471  
 A;Molecule type: protein  
 A;Residues: 1-31 <NGU>  
 A;Experimental source: pancreas  
 C;Superfamily: glucagon  
 C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas  
 F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 11.8%; Score 4; DB 2; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24  
 ||||  
 Db 23 VEWL 26

# RESULT 11

S44472  
 glucagon G2 - North American paddlefish (*Polyodon spathula*)  
 C;Species: *Polyodon spathula*  
 C;Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 07-May-1999  
 C;Accession: S44472  
 R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 11.8%; Score 4; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24  
|||  
Db 23 VEWL 26

## RESULT 12

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058; TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 11.8%; Score 4; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 26 KKLQ 29

# RESULT 13

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4  
 ||||  
 Db 26 SVSE 29

# RESULT 14

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 11.8%; Score 4; DB 2; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21  
 ||||  
 Db 8 MERV 11

# RESULT 15

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C;Accession: G84161  
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;  
 Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.;  
 Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,  
 R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;  
 Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,  
 J.L.; Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,  
 T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.  
 A;Title: Genome sequence of Halobacterium species NRC-1.  
 A;Reference number: A84160; MUID:20504483; PMID:11016950  
 A;Accession: G84161  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-32 <STO>  
 A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138  
 C;Genetics:  
 A;Gene: VNG0019H

Query Match 11.8%; Score 4; DB 2; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30  
 ||||  
 Db 13 KLQD 16

# RESULT 16

E81714

hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000

C;Accession: E81714

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;  
 Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;  
 Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,  
 W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,  
 C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae  
 AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <TET>

A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;  
 PID:g7190379; GSPDB:GN00121; TIGR:TC0337

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0337

Query Match 11.8%; Score 4; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
|||  
Db 26 LRKK 29

RESULT 17

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4  
|||  
Db 29 SVSE 32

RESULT 18

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4  
|||  
Db 29 SVSE 32

RESULT 19

D82125

hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match 11.8%; Score 4; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 24 KKLQ 27

RESULT 20

S70806

hypothetical protein 5 - *Vibrio cholerae* (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: *Vibrio cholerae*

C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 11.8%; Score 4; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20  
|||  
Db 14 SMER 17

RESULT 21

F95057

hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0497

Query Match 11.8%; Score 4; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 10 KKLQ 13

RESULT 22

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhagen, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 11.8%; Score 4; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 4 KKLQ 7

#### RESULT 23

S46227

hypothetical protein - *Streptomyces chrysomallus* (fragment)

C;Species: *Streptomyces chrysomallus*

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: *Streptomyces chrysomallus* FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 11.8%; Score 4; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22  
|||  
Db 27 ERVE 30

#### RESULT 24

S71912

hemoglobin, extracellular, chain A1 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.  
Biochim. Biophys. Acta 1290, 215-223, 1996  
A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.  
A;Reference number: S71912; MUID:96350431; PMID:8765123  
A;Accession: S71912  
A;Molecule type: protein  
A;Residues: 1-37 <MAT>  
C;Superfamily: globin; globin homology  
C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22  
|||  
Db 25 ERVE 28

RESULT 25

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 11.8%; Score 4; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28  
|||  
Db 6 RKKL 9

RESULT 26

CKFHCS

sarcotoxin IC - flesh fly (*Sarcophaga peregrina*)

C;Species: *Sarcophaga peregrina*

C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997  
A;Accession: C22625  
A;Molecule type: protein  
A;Residues: 1-39 <OKA>  
C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.  
C;Superfamily: cecropin  
C;Keywords: amidated carboxyl end; antibacterial; hemolymph  
F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26  
|||  
Db 2 WLRK 5

RESULT 27

S71913

hemoglobin, extracellular, chain A2 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71913

A;Molecule type: protein

A;Residues: 1-39 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22  
|||  
Db 27 ERVE 30

RESULT 28

S77164

ycf32 protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sml0007

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C;Accession: S77164

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77164

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-39 <KAN>

A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17722.1; PID:g1652803

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: ycf32

C;Superfamily: hypothetical protein ycf32

Query Match 11.8%; Score 4; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31  
|||  
Db 31 LQDV 34

#### RESULT 29

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: *Squalus acanthias* (spiny dogfish)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, *Squalus acanthias*.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
|||  
Db 10 KKL 12

RESULT 30

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake (fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence\_revision 05-Oct-1989 #text\_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7  
|||  
Db 3 IQL 5

RESULT 31

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 23 LNS 25

RESULT 32

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 23 LNS 25

RESULT 33

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Nov-1995 #sequence\_revision 01-Mar-1996 #text\_change 23-Jul-1999

C;Accession: S58386

R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.

Nucleic Acids Res. 23, 3074-3075, 1995

A;Title: A novel method for sequencing members of multi-gene families.

A;Reference number: S58384; MUID:95388532; PMID:7659534

A;Accession: S58386

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-28 <JOH>

A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

A;Note: only a part of the coding sequence is given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21  
|||  
Db 12 ERV 14

RESULT 34

PN0047

signal transduction protein QM0017 - mouse (fragments)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 15-Oct-1999

C;Accession: PN0047

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0047

A;Molecule type: protein

A;Residues: 1-28 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.

C;Superfamily: signal transduction protein DJ-1

C;Keywords: brain

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12  
|||  
Db 14 NLG 16

RESULT 35

S56121

type I DNA methyltransferase M.EcoR124I chain HsdS - Escherichia coli (fragments)

C;Species: Escherichia coli

C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 03-Nov-1995

C;Accession: S56121

R;Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.

J. Mol. Biol. 250, 181-190, 1995

A;Title: Probing the domain structure of the type IC DNA methyltransferase M.EcoR124I by limited proteolysis.

A;Reference number: S56121; MUID:95333175; PMID:7608969

A;Accession: S56121

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <WEB>

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 DVH 32  
|||  
Db 8 DVH 10

RESULT 36

S70894

hypothetical protein 1 - Vibrio anguillarum (fragment)



C;Species: *Vibrio anguillarum*  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
C;Accession: S70894  
R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.  
Mol. Microbiol. 19, 625-637, 1996  
A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen *Vibrio anguillarum*.  
A;Reference number: S70894; MUID:96228710; PMID:8830252  
A;Accession: S70894  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-28 <OTO>  
A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1; PID:g1723992

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 18 LNS 20

RESULT 37

S22469

hypothetical protein 1 - *Prochlorothrix hollandica*

C;Species: *Prochlorothrix hollandica*  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 15-Oct-1999  
C;Accession: S22469; S16850  
R;Greer, K.L.; Golden, S.S.  
Plant Mol. Biol. 19, 355-365, 1992  
A;Title: Conserved relationship between psbH and petBD genes: presence of a shared upstream element in *Prochlorothrix hollandica*.  
A;Reference number: S22469; MUID:92322967; PMID:1623188  
A;Accession: S22469  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-28 <GRE>  
A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3  
|||  
Db 4 SVS 6

RESULT 38

S26254

rel protein - chicken

C;Species: *Gallus gallus* (chicken)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 06-Dec-1996  
C;Accession: S26254  
R;Capobianco, A.J.; Gilmore, T.D.

Oncogene 6, 2203-2210, 1991

A;Title: Repression of the chicken c-rel promoter by vRel in chicken embryo fibroblasts is not mediated through a consensus NF-kappaB binding site.

A;Reference number: S26254; MUID:92115319; PMID:1766669

A;Accession: S26254

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-28 <CAP>

A;Cross-references: EMBL:X59588

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22  
|||  
Db 1 RVE 3

RESULT 39

I59477

antigen, T-cell receptor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000

C;Accession: I59477

R;Mathioudakis, G.; Chen, P.

Scand. J. Immunol. 38, 31-36, 1993

A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the T-cell antigen receptor to J gamma 2C gamma 2 gene segments in peripheral blood lymphocyte transcripts from normal donors.

A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:g181658

C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
|||  
Db 10 KKL 12

RESULT 40

F46522

T-cell receptor eta chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C;Accession: F46522; I56191

R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Weissman, A.M.

J. Immunol. 150, 122-130, 1993

A;Title: T cell antigen receptor-eta subunit. Low levels of expression and limited cross-species conservation.  
 A;Reference number: A46522; MUID:93107707; PMID:8417118  
 A;Accession: F46522  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: nucleic acid  
 A;Residues: 1-28 <JEN>  
 A;Cross-references: GB:S51404; NID:g262180; PIDN:AAB24606.1; PID:g262181  
 A;Note: sequence extracted from NCBI backbone (NCBIP:120909)  
 R;Itoh, Y.; Matsuura, A.; Kinebuchi, M.; Honda, R.; Takayama, S.; Ichimiya, S.; Kon, S.; Kikuchi, K.  
 J. Immunol. 151, 4705-4717, 1993  
 A;Title: Structural analysis of the CD3 zeta/eta locus of the rat. Expression of zeta but eta transcripts by rat T cells.  
 A;Reference number: I56191; MUID:94014415; PMID:8409430  
 A;Accession: I56191  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-28 <RES>  
 A;Cross-references: GB:D13556; NID:g436580; PIDN:BAA02754.1; PID:g436581  
 C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27  
 |||  
 Db 13 RKK 15

Search completed: January 14, 2004, 10:37:20  
 Job time : 22.0623 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 22.8785 Seconds  
(without alignments)  
303.882 Million cell updates/sec

Title: US-09-843-221A-161  
Perfect score: 34  
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
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#### SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	34	100.0	34	9	US-09-169-786-3	Sequence 3, Appli
2	34	100.0	34	10	US-09-928-047B-6	Sequence 6, Appli
3	34	100.0	34	11	US-09-843-221A-16	Sequence 16, Appl
4	34	100.0	34	11	US-09-843-221A-161	Sequence 161, App
5	34	100.0	34	12	US-09-928-048A-6	Sequence 6, Appli
6	34	100.0	34	12	US-10-361-928-8	Sequence 8, Appli
7	34	100.0	34	12	US-10-340-484-15	Sequence 15, Appl
8	34	100.0	34	12	US-10-340-484-16	Sequence 16, Appl
9	34	100.0	34	14	US-10-016-403-5	Sequence 5, Appli
10	34	100.0	34	14	US-10-097-079-1	Sequence 1, Appli
11	34	100.0	37	12	US-10-168-185-9	Sequence 9, Appli
12	34	100.0	38	9	US-09-169-786-4	Sequence 4, Appli
13	34	100.0	38	11	US-09-843-221A-14	Sequence 14, Appl
14	34	100.0	38	12	US-10-245-707-1	Sequence 1, Appli
15	33	97.1	33	12	US-10-361-928-9	Sequence 9, Appli
16	33	97.1	34	11	US-09-843-221A-20	Sequence 20, Appl
17	33	97.1	34	12	US-10-361-928-1	Sequence 1, Appli
18	33	97.1	34	12	US-10-361-928-2	Sequence 2, Appli
19	33	97.1	34	12	US-10-361-928-5	Sequence 5, Appli
20	33	97.1	37	11	US-09-843-221A-15	Sequence 15, Appl
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22	32	94.1	33	12	US-10-361-928-6	Sequence 6, Appli
23	31	91.2	31	9	US-09-169-786-2	Sequence 2, Appli
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263	4	11.8	35	11	US-09-983-802-486	Sequence 486, App
264	4	11.8	35	11	US-09-820-843A-106	Sequence 106, App
265	4	11.8	35	11	US-09-925-299-1258	Sequence 1258, Ap
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267	4	11.8	35	12	US-10-340-484-13	Sequence 13, Appl
268	4	11.8	35	12	US-10-012-952A-147	Sequence 147, App
269	4	11.8	35	12	US-10-062-599-138	Sequence 138, App
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271	4	11.8	35	15	US-10-062-831-138	Sequence 138, App
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298	4	11.8	37	12	US-10-340-783-16	Sequence 16, Appl
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818	3	8.8	28	15	US-10-187-051-117	Sequence 117, App
819	3	8.8	28	15	US-10-187-051-119	Sequence 119, App
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831	3	8.8	28	15	US-10-187-051-143	Sequence 143, App
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834	3	8.8	28	15	US-10-187-051-149	Sequence 149, App
835	3	8.8	28	15	US-10-187-051-151	Sequence 151, App
836	3	8.8	28	15	US-10-187-051-155	Sequence 155, App
837	3	8.8	28	15	US-10-187-051-163	Sequence 163, App
838	3	8.8	28	15	US-10-187-051-165	Sequence 165, App
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840	3	8.8	28	15	US-10-023-282-638	Sequence 638, App
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844	3	8.8	28	15	US-10-202-724-3	Sequence 3, Appli
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852	3	8.8	28	15	US-10-197-954-62	Sequence 62, Appl
853	3	8.8	28	15	US-10-197-954-145	Sequence 145, App
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916	3	8.8	29	9	US-09-881-490-3	Sequence 3, Appli
917	3	8.8	29	9	US-09-789-836-13	Sequence 13, Appl
918	3	8.8	29	10	US-09-927-112-5	Sequence 5, Appli
919	3	8.8	29	10	US-09-927-112-6	Sequence 6, Appli
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932	3	8.8	29	10	US-09-911-969-7	Sequence 7, Appli
933	3	8.8	29	10	US-09-880-149-52	Sequence 52, Appl
934	3	8.8	29	10	US-09-880-149-55	Sequence 55, Appl
935	3	8.8	29	10	US-09-764-877-1395	Sequence 1395, Ap
936	3	8.8	29	10	US-09-867-852-152	Sequence 152, App
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939	3	8.8	29	10	US-09-956-206A-1	Sequence 1, Appli
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943	3	8.8	29	11	US-09-956-940-38	Sequence 38, Appl
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953	3	8.8	29	11	US-09-847-102A-80	Sequence 80, Appl
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957	3	8.8	29	11	US-09-983-966-227	Sequence 227, App
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959	3	8.8	29	11	US-09-764-891-4191	Sequence 4191, Ap
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961	3	8.8	29	11	US-09-892-877-436	Sequence 436, App
962	3	8.8	29	11	US-09-847-208-125	Sequence 125, App
963	3	8.8	29	11	US-09-305-736-406	Sequence 406, App
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966	3	8.8	29	11	US-09-305-736-581	Sequence 581, App
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970	3	8.8	29	11	US-09-491-614-14	Sequence 14, Appl
971	3	8.8	29	11	US-09-491-614-15	Sequence 15, Appl
972	3	8.8	29	11	US-09-948-783-438	Sequence 438, App
973	3	8.8	29	11	US-09-910-082A-158	Sequence 158, App
974	3	8.8	29	11	US-09-910-082A-368	Sequence 368, App
975	3	8.8	29	12	US-10-153-604A-72	Sequence 72, Appl
976	3	8.8	29	12	US-10-231-894-44	Sequence 44, Appl
977	3	8.8	29	12	US-10-345-281-52	Sequence 52, Appl
978	3	8.8	29	12	US-10-345-281-55	Sequence 55, Appl
979	3	8.8	29	12	US-10-234-816-95	Sequence 95, Appl
980	3	8.8	29	12	US-09-789-831-13	Sequence 13, Appl
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982	3	8.8	29	12	US-09-935-384-758	Sequence 758, App
983	3	8.8	29	12	US-10-131-909A-4	Sequence 4, Appli
984	3	8.8	29	12	US-10-131-909A-7	Sequence 7, Appli
985	3	8.8	29	12	US-10-096-777-1	Sequence 1, Appli
986	3	8.8	29	12	US-10-008-524A-123	Sequence 123, App
987	3	8.8	29	12	US-10-340-458-4	Sequence 4, Appli
988	3	8.8	29	12	US-10-340-458-21	Sequence 21, Appl
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990	3	8.8	29	12	US-09-963-693-71	Sequence 71, Appl
991	3	8.8	29	12	US-10-105-232-319	Sequence 319, App
992	3	8.8	29	12	US-10-105-232-512	Sequence 512, App
993	3	8.8	29	12	US-10-280-066-334	Sequence 334, App
994	3	8.8	29	12	US-10-289-135A-25	Sequence 25, Appl
995	3	8.8	29	12	US-10-029-386-27545	Sequence 27545, A
996	3	8.8	29	12	US-10-029-386-27995	Sequence 27995, A
997	3	8.8	29	12	US-10-029-386-29238	Sequence 29238, A
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999	3	8.8	29	12	US-10-029-386-30256	Sequence 30256, A
1000	3	8.8	29	12	US-10-029-386-31071	Sequence 31071, A

#### ALIGNMENTS

##### RESULT 1

US-09-169-786-3

; Sequence 3, Application US/09169786B

; Patent No. US20020025929A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Masahiko

; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE

; FILE REFERENCE: X-11480

; CURRENT APPLICATION NUMBER: US/09/169,786B

; CURRENT FILING DATE: 1998-10-09

; EARLIER APPLICATION NUMBER: US 60/061,800

; EARLIER FILING DATE: 1997-10-14

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-169-786-3

Query Match 100.0%; Score 34; DB 9; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

US-09-928-047B-6

; Sequence 6, Application US/09928047B  
; Patent No. US20020160945A1  
; GENERAL INFORMATION:  
; APPLICANT: Cantor, Thomas  
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE  
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS  
; FILE REFERENCE: 53221-20002.00  
; CURRENT APPLICATION NUMBER: US/09/928,047B  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US 60/224,446  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-047B-6

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Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

US-09-843-221A-16

; Sequence 16, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28

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; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-16
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Query Match 100.0%; Score 34; DB 11; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

## RESULT 4

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US-09-843-221A-161
; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-161

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Query Match 100.0%; Score 34; DB 11; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
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US-09-928-048A-6  
; Sequence 6, Application US/09928048A  
; Publication No. US20030138858A1  
; GENERAL INFORMATION:  
; APPLICANT: Scantibodies Laboratory, Inc.  
; APPLICANT: Cantor, Thomas L.  
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT  
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20015.00  
; CURRENT APPLICATION NUMBER: US/09/928,048A  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-928-048A-6

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RESULT 6

US-10-361-928-8  
; Sequence 8, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; TITLE OF INVENTION: ANALOGS  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: 09/447,800  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/110,152  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Desamino Ser  
US-10-361-928-8

Query Match 100.0%; Score 34; DB 12; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

US-10-340-484-15  
; Sequence 15, Application US/10340484  
; Publication No. US20030171288A1  
; GENERAL INFORMATION:  
; APPLICANT: Stewart, Andrew F.  
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic  
; TITLE OF INVENTION: Drugs  
; FILE REFERENCE: 25200-501  
; CURRENT APPLICATION NUMBER: US/10/340,484  
; CURRENT FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: 60/347,215  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: 60/353,296  
; PRIOR FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: 60/368,955  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: 60/379,125  
; PRIOR FILING DATE: 2002-05-08  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-340-484-15

Query Match 100.0%; Score 34; DB 12; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-10-340-484-16  
; Sequence 16, Application US/10340484  
; Publication No. US20030171288A1  
; GENERAL INFORMATION:  
; APPLICANT: Stewart, Andrew F.  
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic

```

; TITLE OF INVENTION:  Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

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```

Query Match          100.0%; Score 34; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

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# RESULT 9

US-10-016-403-5

```

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06

```

; ATTORNEY/AGENT INFORMATION:  
; NAME: Frenchick, Grady J.  
; REGISTRATION NUMBER: 29,018  
; REFERENCE/DOCKET NUMBER: 8734.28  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-257-2281  
; TELEFAX: 608-257-7643  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..34  
; OTHER INFORMATION: /note= "parathyroid hormone"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-016-403-5

Query Match 100.0%; Score 34; DB 14; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.4e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 10

US-10-097-079-1

; Sequence 1, Application US/10097079  
; Publication No. US20020132973A1  
; GENERAL INFORMATION:  
; APPLICANT: Condon, Stephen M.  
; Morize, Isabelle  
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/097,079  
; FILING DATE: 13-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/228,990  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 60/046,472

```

; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: No. US20020132973A1 Relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-079-1

```

```

Query Match          100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 11

US-10-168-185-9

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; Sequence 9, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-9

```

```

Query Match          100.0%; Score 34; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 12

US-09-169-786-4

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; Sequence 4, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-4

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```

Query Match          100.0%; Score 34; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 7e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 13

US-09-843-221A-14

```

; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 14  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-14

Query Match 100.0%; Score 34; DB 11; Length 38;  
Best Local Similarity 100.0%; Pred. No. 7e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

US-10-245-707-1

; Sequence 1, Application US/10245707  
; Publication No. US20030171282A1  
; GENERAL INFORMATION:  
; APPLICANT: Patton, John S.  
; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments of Parathyroid Hormone

; FILE REFERENCE: 032055-047  
; CURRENT APPLICATION NUMBER: US/10/245,707  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 09/577,264  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 09/128,401  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: US 08/625,586  
; PRIOR FILING DATE: 1996-03-28  
; PRIOR APPLICATION NUMBER: US 08/232,849  
; PRIOR FILING DATE: 1994-04-25  
; PRIOR APPLICATION NUMBER: US 07/953,397  
; PRIOR FILING DATE: 1992-09-29  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1

; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: parathyroid hormone (PTH) fragment molecules  
US-10-245-707-1

Query Match 100.0%; Score 34; DB 12; Length 38;  
Best Local Similarity 100.0%; Pred. No. 7e-28;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-10-361-928-9

```

; Sequence 9, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-9

```

```

Query Match          97.1%; Score 33; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.6e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

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RESULT 16
US-09-843-221A-20
; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170

```



; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified human PTH  
US-09-843-221A-20

Query Match 97.1%; Score 33; DB 11; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.7e-27;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-10-361-928-1

; Sequence 1, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; TITLE OF INVENTION: ANALOGS  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: 09/447,800  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/110,152  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (1)  
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly  
US-10-361-928-1

Query Match 97.1%; Score 33; DB 12; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.7e-27;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-10-361-928-2

; Sequence 2, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; TITLE OF INVENTION: ANALOGS  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: 09/447,800  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/110,152  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Desamino Gly

US-10-361-928-2

Query Match 97.1%; Score 33; DB 12; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.7e-27;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-10-361-928-5

; Sequence 5, Application US/10361928  
; Publication No. US20030144209A1  
; GENERAL INFORMATION:  
; APPLICANT: BRINGHURST, F. RICHARD  
; APPLICANT: TAKASU, HISASHI  
; APPLICANT: GARDELLA, THOMAS J.  
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)  
; TITLE OF INVENTION: ANALOGS  
; FILE REFERENCE: 0609.4630002  
; CURRENT APPLICATION NUMBER: US/10/361,928  
; CURRENT FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: 09/447,800  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/110,152  
; PRIOR FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5

; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Desamino Ala  
US-10-361-928-5

Query Match 97.1%; Score 33; DB 12; Length 34;  
Best Local Similarity 100.0%; Pred. No. 6.7e-27;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

US-09-843-221A-15  
; Sequence 15, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-15

Query Match 97.1%; Score 33; DB 11; Length 37;  
Best Local Similarity 100.0%; Pred. No. 7.2e-27;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 33

RESULT 21

US-10-361-928-3

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; Sequence 3, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-3

```

```

Query Match          94.1%; Score 32; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 7e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33
        ||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

```

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RESULT 22
US-10-361-928-6
; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

```

Query Match 94.1%; Score 32; DB 12; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7e-26;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33  
 |||  
 Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

RESULT 23

US-09-169-786-2

; Sequence 2, Application US/09169786B

; Patent No. US20020025929A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Masahiko

; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE

; FILE REFERENCE: X-11480

CURRENT APPLICATION NUMBER: US/09/169,786B

; CURRENT FILING DATE: 1998-10-09

; EARLIER APPLICATION NUMBER: US 60/061,800

; EARLIER FILING DATE: 1997-10-14

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEO ID NO 2

; LENGTH: 31

; TYPE: PRT

ORGANISM: Homo sapiens

US-09-169-786-2

Query Match 91.2%; Score 31; DB 9; Length 31;  
Best Local Similarity 100.0%; Pred. No. 7e-25;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV    31  
               |||||  
Db            1 SVSEIOLMHNLGKHLNSMERVEWLRKKLODV    31

RESULT 24

US-09-843-221A-27

; Sequence 27, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

```
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-27
```

```
Query Match          91.2%; Score 31; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          |||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
```

# RESULT 25

US-09-843-221A-165

```
; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
```

US-09-843-221A-165

Query Match 91.2%; Score 31; DB 11; Length 31;  
Best Local Similarity 100.0%; Pred. No. 7e-25;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 26

US-09-843-221A-39

; Sequence 39, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-39

Query Match 88.2%; Score 30; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.3e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30  
|||||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 27

US-09-843-221A-166

; Sequence 166, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE

```

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

```

```

Query Match          88.2%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.3e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

```

# RESULT 28

```

US-09-843-221A-51
; Sequence 51, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51

```



; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-51

Query Match 85.3%; Score 29; DB 11; Length 29;  
Best Local Similarity 100.0%; Pred. No. 7.5e-23;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 29

US-09-843-221A-167

; Sequence 167, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 167  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred embodiments - PTH  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional  
linker  
US-09-843-221A-167

Query Match 85.3%; Score 29; DB 11; Length 29;  
Best Local Similarity 100.0%; Pred. No. 7.5e-23;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29  
|||  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 30

US-09-843-221A-43

```
; Sequence 43, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-43
```

```
Query Match      85.3%; Score 29; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.7e-23;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
        |||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
```

RESULT 31

US-10-372-095-24

```
; Sequence 24, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
```

; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-372-095-24

Query Match 85.3%; Score 29; DB 12; Length 34;  
Best Local Similarity 100.0%; Pred. No. 8.5e-23;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQLMHNLGKHLNSMERVEWLRKKLQDVH 32  
|||  
Db 4 EIQLMHNLGKHLNSMERVEWLRKKLQDVH 32

RESULT 32

US-09-843-221A-32  
; Sequence 32, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-221A-32

Query Match 82.4%; Score 28; DB 11; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.7e-22;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
|||  
Db 1 LMHNLGKHLNSMERVEWLRKKLQDVHNF 28

RESULT 33

US-09-843-221A-52  
; Sequence 52, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL

```

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-52

```

```

Query Match          82.4%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.7e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        ||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

```

# RESULT 34

```

US-09-843-221A-168
; Sequence 168, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence

```



; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..34  
; OTHER INFORMATION: /note= "modified parathyroid  
; hormone"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-016-403-6

Query Match 82.4%; Score 28; DB 14; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9e-22;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 LMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

US-10-016-403-7

; Sequence 7, Application US/10016403  
; Publication No. US20020107505A1  
; GENERAL INFORMATION:  
; APPLICANT: Holladay, Leslie A.  
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO  
; INCREASE ELECTROTRANSPORT FLUX  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard  
; STREET: 25 West Main Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: USA  
; ZIP: 53701-2236  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/016,403  
; FILING DATE: 10-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466,610  
; FILING DATE: 1995-JUN-06  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frenchick, Grady J.  
; REGISTRATION NUMBER: 29,018  
; REFERENCE/DOCKET NUMBER: 8734.28  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-257-2281  
; TELEFAX: 608-257-7643  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

```

;           FEATURE:
;           NAME/KEY:  Peptide
;           LOCATION:  1..34
;           OTHER INFORMATION:  /note= "modified parathyroid
;           hormone"
;           SEQUENCE DESCRIPTION:  SEQ ID NO: 7:
US-10-016-403-7

```

```

Query Match          82.4%;  Score 28;  DB 14;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 9e-22;
Matches 28;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY          1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
             ||||||||||||||||||||||||||||
Db          1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

```

```

RESULT 37
US-09-843-221A-50
; Sequence 50, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-50

```

```

Query Match          76.5%;  Score 26;  DB 11;  Length 30;
Best Local Similarity 100.0%;  Pred. No. 9.2e-20;
Matches 26;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY          1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
             ||||||||||||||||||||||||
Db          1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

```

RESULT 38

US-09-843-221A-28

; Sequence 28, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified human PTH

US-09-843-221A-28

Query Match 76.5%; Score 26; DB 11; Length 31;  
Best Local Similarity 100.0%; Pred. No. 9.4e-20;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26  
| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 39

US-10-031-874A-206

; Sequence 206, Application US/10031874A  
; Publication No. US20030190598A1  
; GENERAL INFORMATION:  
; APPLICANT: TANHA, JAMSHID  
; APPLICANT: DUBUC, GINETTE  
; APPLICANT: NARANG, SARAN  
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS  
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES  
; FILE REFERENCE: 11054-1  
; CURRENT APPLICATION NUMBER: US/10/031,874A  
; CURRENT FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/207,234  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 206  
; LENGTH: 31



; TYPE: PRT  
; ORGANISM: Lama glama  
US-10-031-874A-206

Query Match 76.5%; Score 26; DB 12; Length 31;  
Best Local Similarity 100.0%; Pred. No. 9.4e-20;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26  
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 40

US-09-843-221A-17  
; Sequence 17, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND  
PARATHYROID HORMONE-  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified human PTH  
US-09-843-221A-17

Query Match 67.6%; Score 23; DB 11; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 11:15:02  
Job time : 23.8785 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 25.4206 Seconds  
(without alignments)  
345.145 Million cell updates/sec

Title: US-09-843-221A-161  
Perfect score: 34  
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28  
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description
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1	14	41.2	31	11	Q91Y90	Q91y90 peromyscus
2	14	41.2	31	11	Q91Y91	Q91y91 peromyscus
3	5	14.7	34	5	O17148	O17148 echinococcu
4	5	14.7	34	16	Q97K50	Q97k50 clostridium
5	5	14.7	34	17	Q9HR65	Q9hr65 halobacteri
6	5	14.7	35	11	Q8BTB9	Q8btb9 mus musculu
7	5	14.7	35	16	Q97RG6	Q97rg6 streptococc
8	4	11.8	28	10	O24285	O24285 pinus radia
9	4	11.8	28	10	Q8GZQ8	Q8gzz8 hordeum vul
10	4	11.8	29	2	Q49148	Q49148 methylobact
11	4	11.8	29	4	Q9UCL2	Q9ucl2 homo sapien
12	4	11.8	29	4	Q96PP3	Q96pp3 homo sapien
13	4	11.8	29	5	Q25603	Q25603 onchocerca
14	4	11.8	29	8	Q9TI61	Q9ti61 allosyncarp
15	4	11.8	29	13	O13043	O13043 scyliorhinu
16	4	11.8	30	2	Q9JMV3	Q9jmv3 escherichia
17	4	11.8	30	4	Q9UBV5	Q9ubv5 homo sapien
18	4	11.8	30	16	Q8DZP7	Q8dzz7 streptococc
19	4	11.8	31	1	Q55314	Q55314 sulfolobus
20	4	11.8	31	4	Q8NEI8	Q8nei8 homo sapien
21	4	11.8	31	8	Q9MS77	Q9ms77 phacus acum
22	4	11.8	31	16	O50669	O50669 borrelia bu
23	4	11.8	32	11	Q9QZQ2	Q9qzz2 mus musculu
24	4	11.8	32	17	Q9HSZ0	Q9hsz0 halobacteri
25	4	11.8	33	5	Q95SD4	Q95sd4 drosophila
26	4	11.8	33	16	Q9PKX3	Q9pkx3 chlamydia m
27	4	11.8	34	2	Q9ZG81	Q9zg81 chlamydia t
28	4	11.8	34	2	Q8GFK2	Q8gfk2 staphylococ
29	4	11.8	34	11	Q8C4P4	Q8c4p4 mus musculu
30	4	11.8	34	13	Q90ZJ4	Q90zj4 gallus gall
31	4	11.8	34	16	Q98FK5	Q98fk5 rhizobium l
32	4	11.8	34	16	Q8G2Q2	Q8g2q2 brucella su
33	4	11.8	35	4	Q15421	Q15421 homo sapien
34	4	11.8	35	12	Q8V6J8	Q8v6j8 halovirus h
35	4	11.8	35	16	Q9KQG4	Q9kqg4 vibrio chol
36	4	11.8	35	16	Q8F102	Q8f102 leptospira
37	4	11.8	36	2	Q53920	Q53920 streptomyce
38	4	11.8	36	2	O68941	O68941 rhodospiril
39	4	11.8	36	4	Q8WXW8	Q8wxw8 homo sapien
40	4	11.8	36	10	Q9SJ63	Q9sj63 arabidopsis
41	4	11.8	36	12	Q9PXD1	Q9pxd1 hepatitis c
42	4	11.8	36	12	Q91D77	Q91d77 ttv-like mi
43	4	11.8	36	13	Q9YHT9	Q9yht9 brachydanio
44	4	11.8	36	16	Q97S91	Q97s91 streptococc
45	4	11.8	37	2	Q8KYJ0	Q8kyj0 bacillus an
46	4	11.8	37	5	Q9N2L2	Q9n2l2 caenorhabdi
47	4	11.8	37	10	Q39942	Q39942 helianthus
48	4	11.8	37	13	Q8AWW8	Q8aww8 oncorhynchu
49	4	11.8	37	16	Q8F6U2	Q8f6u2 leptospira
50	4	11.8	37	16	Q8F5H3	Q8f5h3 leptospira
51	4	11.8	37	16	Q8F419	Q8f419 leptospira
52	4	11.8	37	16	Q8EXV9	Q8exv9 leptospira
53	4	11.8	38	2	Q8KWH7	Q8kwh7 lactobacill
54	4	11.8	38	5	Q9NBE3	Q9nbe3 chironomus
55	4	11.8	38	5	Q9NBE5	Q9nbe5 chironomus
56	4	11.8	38	5	Q9NBE8	Q9nbe8 chironomus
57	4	11.8	38	5	Q9NBE4	Q9nbe4 chironomus

58	4	11.8	38	5	Q9NBE7	Q9nbe7 chironomus
59	4	11.8	38	11	Q91VC8	Q91vc8 mus musculu
60	4	11.8	38	13	Q8AWW9	Q8aww9 oncorhynchu
61	4	11.8	38	16	Q8E0D2	Q8e0d2 streptococc
62	4	11.8	39	2	Q8GPQ8	Q8gppq8 pseudomonas
63	4	11.8	39	10	Q9FEY1	Q9fey1 heterocapsa
64	4	11.8	39	12	Q68847	Q68847 hepatitis c
65	4	11.8	39	12	Q68845	Q68845 hepatitis c
66	4	11.8	39	12	Q68846	Q68846 hepatitis c
67	4	11.8	39	13	Q90776	Q90776 gallus gall
68	4	11.8	39	16	Q9KYH4	Q9kyh4 streptomyce
69	4	11.8	39	16	Q8F0C7	Q8f0c7 leptospira
70	4	11.8	39	16	Q8EZ33	Q8ez33 leptospira
71	4	11.8	40	2	Q8GCS7	Q8gcs7 eubacterium
72	4	11.8	40	4	P78340	P78340 homo sapien
73	4	11.8	40	6	Q29283	Q29283 sus scrofa
74	4	11.8	40	10	Q8H192	Q8h192 arabidopsis
75	4	11.8	40	12	Q91JZ7	Q91jz7 hepatitis c
76	4	11.8	40	12	Q8V647	Q8v647 rabies viru
77	3	8.8	28	2	Q01303	Q01303 treponema p
78	3	8.8	28	2	Q05574	Q05574 prochloroth
79	3	8.8	28	2	Q9ZB83	Q9zb83 vibrio angu
80	3	8.8	28	3	Q8TGT8	Q8tgt8 saccharomyc
81	3	8.8	28	4	Q96SD9	Q96sd9 homo sapien
82	3	8.8	28	4	Q16326	Q16326 homo sapien
83	3	8.8	28	4	Q96EU0	Q96eu0 homo sapien
84	3	8.8	28	4	O75980	O75980 homo sapien
85	3	8.8	28	4	O95737	O95737 homo sapien
86	3	8.8	28	5	Q8MUW0	Q8muw0 schistosoma
87	3	8.8	28	5	Q8MPY2	Q8mpy2 caenorhabdi
88	3	8.8	28	5	Q9BM68	Q9bm68 glottidia p
89	3	8.8	28	5	Q9BJE4	Q9bje4 pauropus sp
90	3	8.8	28	6	O62821	O62821 bubalus bub
91	3	8.8	28	6	Q9XS89	Q9xs89 equus cabal
92	3	8.8	28	8	Q8WBC8	Q8wbc8 cucurbita e
93	3	8.8	28	8	Q9TIE9	Q9tie9 centella er
94	3	8.8	28	8	Q9TIE8	Q9tie8 centella as
95	3	8.8	28	8	Q9MR96	Q9mr96 crocodylus
96	3	8.8	28	8	Q9TIE6	Q9tie6 centella hi
97	3	8.8	28	8	Q9ZYS4	Q9zys4 leishmania
98	3	8.8	28	8	Q9MR94	Q9mr94 chelonias my
99	3	8.8	28	8	Q9TIE7	Q9tie7 centella tr
100	3	8.8	28	8	Q8HS23	Q8hs23 pisum sativ
101	3	8.8	28	8	Q8HS11	Q8hs11 spathiphyll
102	3	8.8	28	8	Q8HS07	Q8hs07 welwitschia
103	3	8.8	28	8	Q8HKF0	Q8hkf0 rhipicephal
104	3	8.8	28	9	Q9AZJ9	Q9azj9 bacterioph
105	3	8.8	28	9	Q38269	Q38269 bacterioph
106	3	8.8	28	10	Q8S526	Q8s526 ipomoea bat
107	3	8.8	28	10	Q8W232	Q8w232 zea mays (m
108	3	8.8	28	10	Q9LMD6	Q9lmd6 arabidopsis
109	3	8.8	28	10	Q944P1	Q944p1 manihot esc
110	3	8.8	28	11	Q9ESI4	Q9esi4 petromus ty
111	3	8.8	28	11	Q9ESI5	Q9esi5 thryonomys
112	3	8.8	28	11	Q9ESI6	Q9esi6 hystrix afr
113	3	8.8	28	11	Q99PL9	Q99pl9 mus musculu
114	3	8.8	28	11	Q9ESI2	Q9esi2 cryptomys h

115	3	8.8	28	11	Q9EP60	Q9ep60 heliophobiu
116	3	8.8	28	11	Q9ESI0	Q9esi0 cryptomys s
117	3	8.8	28	11	Q91XP0	Q91xp0 rattus norv
118	3	8.8	28	11	P70651	P70651 mus sp. bet
119	3	8.8	28	11	Q9EP59	Q9ep59 georychus c
120	3	8.8	28	11	Q9ESI1	Q9esi1 cryptomys d
121	3	8.8	28	11	P97914	P97914 rattus norv
122	3	8.8	28	11	Q9EP61	Q9ep61 heteroceph
123	3	8.8	28	11	Q9ESH8	Q9esh8 bathyergus
124	3	8.8	28	11	Q9ESH9	Q9esh9 bathyergus
125	3	8.8	28	11	Q9QXB4	Q9qxb4 mus musculu
126	3	8.8	28	11	Q9ESI3	Q9esi3 cryptomys h
127	3	8.8	28	12	Q68087	Q68087 hepatitis c
128	3	8.8	28	12	Q67786	Q67786 human adeno
129	3	8.8	28	12	Q68095	Q68095 hepatitis c
130	3	8.8	28	12	Q68097	Q68097 hepatitis c
131	3	8.8	28	12	Q68092	Q68092 hepatitis c
132	3	8.8	28	12	Q68091	Q68091 hepatitis c
133	3	8.8	28	12	Q68093	Q68093 hepatitis c
134	3	8.8	28	12	Q68099	Q68099 hepatitis c
135	3	8.8	28	12	Q68096	Q68096 hepatitis c
136	3	8.8	28	12	Q68098	Q68098 hepatitis c
137	3	8.8	28	12	Q83181	Q83181 cauliflower
138	3	8.8	28	12	Q68086	Q68086 hepatitis c
139	3	8.8	28	12	Q68552	Q68552 hepatitis c
140	3	8.8	28	12	Q68094	Q68094 hepatitis c
141	3	8.8	28	12	Q9WNI4	Q9wni4 tt virus. o
142	3	8.8	28	13	Q9PRE8	Q9pre8 oryzias lat
143	3	8.8	28	13	Q9PRI9	Q9pri9 amia calva
144	3	8.8	28	13	Q9PRN8	Q9prn8 carassius a
145	3	8.8	28	15	O71346	O71346 human endog
146	3	8.8	28	15	Q9QEY3	Q9qey3 human immun
147	3	8.8	28	16	Q8X415	Q8x415 escherichia
148	3	8.8	28	16	Q8NVB8	Q8nvb8 staphylococ
149	3	8.8	28	16	Q8ENT7	Q8ent7 oceanobacil
150	3	8.8	28	16	Q8CK95	Q8ck95 yersinia pe
151	3	8.8	29	2	Q9ZGG4	Q9zgg4 heliobacill
152	3	8.8	29	2	Q54200	Q54200 streptomyce
153	3	8.8	29	2	Q9X3E3	Q9x3e3 prochloroco
154	3	8.8	29	2	Q9X3J9	Q9x3j9 prochloroco
155	3	8.8	29	2	Q47650	Q47650 escherichia
156	3	8.8	29	2	Q9AKV1	Q9akv1 neisseria g
157	3	8.8	29	2	Q9R526	Q9r526 vibrio chol
158	3	8.8	29	3	P78747	P78747 saccharomyc
159	3	8.8	29	3	Q8TGQ5	Q8tgq5 saccharomyc
160	3	8.8	29	4	Q9Y3G1	Q9y3g1 homo sapien
161	3	8.8	29	4	Q9H2A1	Q9h2a1 homo sapien
162	3	8.8	29	4	Q9UN87	Q9un87 homo sapien
163	3	8.8	29	4	Q9H465	Q9h465 homo sapien
164	3	8.8	29	4	Q8NEF6	Q8nef6 homo sapien
165	3	8.8	29	4	Q8TDW8	Q8tdw8 homo sapien
166	3	8.8	29	4	Q96IR5	Q96ir5 homo sapien
167	3	8.8	29	4	Q9BSQ3	Q9bsq3 homo sapien
168	3	8.8	29	5	Q95VB2	Q95vb2 spirometra
169	3	8.8	29	5	Q95NF4	Q95nf4 drosophila
170	3	8.8	29	5	Q24683	Q24683 dugesia tig
171	3	8.8	29	5	Q8T936	Q8t936 folsomia ca

172	3	8.8	29	6	Q9TRG5	Q9trg5	sus	scrofa
173	3	8.8	29	8	Q8WBB9	Q8wbb9	cucurbita	f
174	3	8.8	29	8	Q9TI57	Q9ti57	corymbia	pa
175	3	8.8	29	8	Q8W7W7	Q8w7w7	cucurbita	p
176	3	8.8	29	8	Q9GF70	Q9gf70	trochodendr	
177	3	8.8	29	8	Q8W7W4	Q8w7w4	cucurbita	a
178	3	8.8	29	8	Q8W7W6	Q8w7w6	cucurbita	p
179	3	8.8	29	8	Q8WBC1	Q8wbc1	cucurbita	o
180	3	8.8	29	8	Q9B5Z6	Q9b5z6	pseudostylo	
181	3	8.8	29	8	Q8W7W5	Q8w7w5	cucurbita	p
182	3	8.8	29	8	Q9B938	Q9b938	eupristina	
183	3	8.8	29	8	Q9G370	Q9g370	draco	blanf
184	3	8.8	29	8	Q8WBD0	Q8wbd0	cucurbita	a
185	3	8.8	29	8	Q8WBB6	Q8wbb6	citrullus	l
186	3	8.8	29	8	Q8W7W9	Q8w7w9	cucurbita	f
187	3	8.8	29	8	Q8W7W8	Q8w7w8	cucurbita	m
188	3	8.8	29	8	Q8HS21	Q8hs21	rheum	x cul
189	3	8.8	29	9	Q9FZX6	Q9fzx6	bacterioph	
190	3	8.8	29	10	P82196	P82196	spinacia	ol
191	3	8.8	29	11	Q9Z2C0	Q9z2c0	mus	musculu
192	3	8.8	29	11	Q921Z6	Q921z6	mus	musculu
193	3	8.8	29	11	Q9Z2C1	Q9z2c1	mus	musculu
194	3	8.8	29	11	O70564	O70564	mus	musculu
195	3	8.8	29	11	Q9QY65	Q9qy65	mus	musculu
196	3	8.8	29	11	Q62300	Q62300	mus	musculu
197	3	8.8	29	11	O08980	O08980	mus	musculu
198	3	8.8	29	11	Q8CGM8	Q8cgm8	mus	musculu
199	3	8.8	29	12	Q91HB1	Q91hbl	porcine	cir
200	3	8.8	29	12	O92646	O92646	hepatitis	e
201	3	8.8	29	12	Q919A5	Q919a5	porcine	rep
202	3	8.8	29	12	Q919A7	Q919a7	porcine	rep
203	3	8.8	29	12	Q86872	Q86872	cauliflower	
204	3	8.8	29	12	O92648	O92648	hepatitis	e
205	3	8.8	29	12	O56835	O56835	vibrio	chol
206	3	8.8	29	13	P82235	P82235	rana	tempor
207	3	8.8	29	13	Q8AYR0	Q8ayr0	oryzias	lat
208	3	8.8	29	13	Q8AWC2	Q8awc2	gallus	gall
209	3	8.8	29	15	O72001	O72001	human	endog
210	3	8.8	29	15	O71342	O71342	human	endog
211	3	8.8	29	15	O71339	O71339	human	endog
212	3	8.8	29	15	O71347	O71347	human	endog
213	3	8.8	29	15	O71340	O71340	human	endog
214	3	8.8	29	15	O71343	O71343	human	endog
215	3	8.8	29	15	Q9IQJ8	Q9iqj8	human	immun
216	3	8.8	29	15	O71991	O71991	human	endog
217	3	8.8	29	15	Q9IQJ1	Q9iqj1	human	immun
218	3	8.8	29	15	O71994	O71994	human	endog
219	3	8.8	29	15	O71341	O71341	human	endog
220	3	8.8	29	15	O71345	O71345	human	endog
221	3	8.8	29	15	O71336	O71336	human	endog
222	3	8.8	29	15	O71344	O71344	human	endog
223	3	8.8	29	15	O71338	O71338	human	endog
224	3	8.8	29	15	O71992	O71992	human	endog
225	3	8.8	29	15	O71337	O71337	human	endog
226	3	8.8	29	15	Q9IQJ9	Q9iqj9	human	immun
227	3	8.8	29	15	O71997	O71997	human	endog
228	3	8.8	29	15	O71335	O71335	human	endog

229	3	8.8	29	16	Q9JZN6	Q9jzn6 neisseria m
230	3	8.8	29	16	Q8X419	Q8x419 escherichia
231	3	8.8	29	17	Q8Q0H5	Q8q0h5 methanosarc
232	3	8.8	30	2	Q9JP75	Q9jp75 salmonella
233	3	8.8	30	2	Q9L8W9	Q9l8w9 streptomyce
234	3	8.8	30	2	Q9L8X1	Q9l8x1 streptomyce
235	3	8.8	30	2	Q9R4Z6	Q9r4z6 clostridium
236	3	8.8	30	2	Q9REI5	Q9rei5 acidiphiliu
237	3	8.8	30	2	Q9R4J2	Q9r4j2 helicobacte
238	3	8.8	30	2	Q8VUW9	Q8vuw9 staphylococ
239	3	8.8	30	2	Q9R4I5	Q9r4i5 mycoplasma
240	3	8.8	30	2	Q9R5Q3	Q9r5q3 leuconostoc
241	3	8.8	30	2	Q93GF6	Q93gf6 staphylococ
242	3	8.8	30	2	Q45966	Q45966 coxiella bu
243	3	8.8	30	2	Q9R5C4	Q9r5c4 comamonas.
244	3	8.8	30	2	Q9R5K3	Q9r5k3 leptospira
245	3	8.8	30	2	Q9R4I6	Q9r4i6 mycoplasma
246	3	8.8	30	2	Q9RER6	Q9rer6 enterobacte
247	3	8.8	30	3	Q8TGM3	Q8tgm3 saccharomyc
248	3	8.8	30	3	Q9URB0	Q9urb0 candida alb
249	3	8.8	30	3	Q8J172	Q8j172 trichoderma
250	3	8.8	30	3	Q8J171	Q8j171 hypocrea li
251	3	8.8	30	4	Q16330	Q16330 homo sapien
252	3	8.8	30	4	O95595	O95595 homo sapien
253	3	8.8	30	4	P78460	P78460 homo sapien
254	3	8.8	30	4	Q8N563	Q8n563 homo sapien
255	3	8.8	30	4	P78542	P78542 homo sapien
256	3	8.8	30	4	Q8IU66	Q8iu66 homo sapien
257	3	8.8	30	5	Q8SZJ6	Q8szj6 drosophila
258	3	8.8	30	5	Q9TWH7	Q9twh7 ancylostoma
259	3	8.8	30	5	Q968N1	Q968n1 tritrichomo
260	3	8.8	30	5	P82214	P82214 bombyx mori
261	3	8.8	30	6	Q9BDK1	Q9bdk1 bos taurus
262	3	8.8	30	6	Q9TTF9	Q9ttf9 ateles belz
263	3	8.8	30	8	Q8W7L1	Q8w7l1 cucurbita m
264	3	8.8	30	8	Q8W7K9	Q8w7k9 cucurbita p
265	3	8.8	30	8	Q8W7H8	Q8w7h8 cucurbita a
266	3	8.8	30	8	Q8WBC2	Q8wbc2 cucurbita o
267	3	8.8	30	8	Q8W7K8	Q8w7k8 cucurbita p
268	3	8.8	30	8	Q8W7H6	Q8w7h6 cucurbita m
269	3	8.8	30	8	Q8WBC4	Q8wbc4 cucurbita p
270	3	8.8	30	8	Q8W7L2	Q8w7l2 cucurbita a
271	3	8.8	30	8	Q8WBC6	Q8wbc6 cucurbita a
272	3	8.8	30	8	Q8WBB7	Q8wbb7 sechium edu
273	3	8.8	30	8	Q99328	Q99328 meloidogyne
274	3	8.8	30	8	Q8W7H7	Q8w7h7 cucurbita e
275	3	8.8	30	8	Q8WBC0	Q8wbc0 cucurbita f
276	3	8.8	30	8	Q9T2T8	Q9t2t8 bos taurus
277	3	8.8	30	8	Q8W7L0	Q8w7l0 cucurbita p
278	3	8.8	30	8	Q9TI56	Q9ti56 eucalyptus
279	3	8.8	30	8	Q8HKG1	Q8hkg1 rhipicephal
280	3	8.8	30	9	Q8W674	Q8w674 enterobacte
281	3	8.8	30	10	Q9S8T2	Q9s8t2 cicer ariet
282	3	8.8	30	10	O23933	O23933 flaveria tr
283	3	8.8	30	10	Q8RUD1	Q8rud1 zea mays (m
284	3	8.8	30	10	Q93WY2	Q93wy2 oryza sativ
285	3	8.8	30	11	Q63885	Q63885 mus sp. cys

286	3	8.8	30	11	O88549	O88549 mesocricetu
287	3	8.8	30	11	Q8VDL1	Q8vdl1 mus musculu
288	3	8.8	30	11	Q9QV18	Q9qv18 rattus sp.
289	3	8.8	30	11	Q9QV14	Q9qv14 mus sp. col
290	3	8.8	30	11	Q9QV19	Q9qv19 rattus sp.
291	3	8.8	30	11	Q10753	Q10753 rattus norv
292	3	8.8	30	11	Q8BR32	Q8br32 mus musculu
293	3	8.8	30	12	Q91HB7	Q91hb7 tt virus. o
294	3	8.8	30	12	Q91HC4	Q91hc4 tt virus. o
295	3	8.8	30	12	Q9IJV5	Q9ijv5 norwalk vir
296	3	8.8	30	12	Q86870	Q86870 cauliflower
297	3	8.8	30	12	Q91HC3	Q91hc3 tt virus. o
298	3	8.8	30	12	Q9WLK3	Q9wlk3 hepatitis e
299	3	8.8	30	12	Q91HC0	Q91hc0 tt virus. o
300	3	8.8	30	13	O42551	O42551 brachydanio
301	3	8.8	30	13	Q9PRW0	Q9prw0 struthio ca
302	3	8.8	30	13	Q9PT00	Q9pt00 oncorhynch
303	3	8.8	30	15	Q86599	Q86599 human endog
304	3	8.8	30	15	Q991P5	Q991p5 human immun
305	3	8.8	30	16	O50822	O50822 borrelia bu
306	3	8.8	30	16	Q9X0W9	Q9x0w9 thermotoga
307	3	8.8	30	16	Q9PP53	Q9pp53 campylobact
308	3	8.8	30	16	Q9KU55	Q9ku55 vibrio chol
309	3	8.8	30	16	Q9KT75	Q9kt75 vibrio chol
310	3	8.8	30	16	Q9JWF4	Q9jwf4 neisseria m
311	3	8.8	30	16	Q97SY9	Q97sy9 streptococc
312	3	8.8	30	16	Q97SX5	Q97sx5 streptococc
313	3	8.8	30	16	Q9K1W7	Q9k1w7 chlamydia p
314	3	8.8	30	16	Q8U566	Q8u566 agrobacteri
315	3	8.8	30	16	Q8KE55	Q8ke55 chlorobium
316	3	8.8	30	16	Q93RS7	Q93rs7 streptomyce
317	3	8.8	30	16	Q8G1R1	Q8glr1 brucella su
318	3	8.8	30	16	Q8FZX9	Q8fzx9 brucella su
319	3	8.8	30	16	Q8CU88	Q8cu88 staphylococ
320	3	8.8	30	17	Q8ZZF0	Q8zzf0 pyrobaculum
321	3	8.8	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
322	3	8.8	31	2	Q9S619	Q9s619 prochloroco
323	3	8.8	31	2	Q8KYK0	Q8kyk0 bacillus an
324	3	8.8	31	2	Q9JMV2	Q9jmv2 escherichia
325	3	8.8	31	2	Q9X3C3	Q9x3c3 prochloroco
326	3	8.8	31	2	O68825	O68825 pseudomonas
327	3	8.8	31	2	Q9KH08	Q9kh08 thermus aqu
328	3	8.8	31	2	Q93GF7	Q93gf7 staphylococ
329	3	8.8	31	2	Q47323	Q47323 escherichia
330	3	8.8	31	2	Q9RHF9	Q9rhf9 acinetobact
331	3	8.8	31	2	Q9R4X1	Q9r4x1 treponema d
332	3	8.8	31	2	Q8KYI9	Q8kyi9 bacillus an
333	3	8.8	31	2	Q8RTS5	Q8rts5 uncultured
334	3	8.8	31	2	Q8L3D3	Q8l3d3 colwellia m
335	3	8.8	31	2	Q93PE1	Q93pe1 yersinia ps
336	3	8.8	31	3	O94120	O94120 saccharomyc
337	3	8.8	31	4	Q96A45	Q96a45 homo sapien
338	3	8.8	31	4	Q9UHM9	Q9uhm9 homo sapien
339	3	8.8	31	4	Q9UEA9	Q9uea9 homo sapien
340	3	8.8	31	4	Q8WYF5	Q8wyf5 homo sapien
341	3	8.8	31	4	Q8N5X3	Q8n5x3 homo sapien
342	3	8.8	31	4	Q9BXM4	Q9bxm4 homo sapien



343	3	8.8	31	4	Q9UDE5	Q9ude5	homo sapien
344	3	8.8	31	5	Q8IQV3	Q8iqv3	drosophila
345	3	8.8	31	5	Q8IEY3	Q8iey3	trypanosoma
346	3	8.8	31	6	Q8MI94	Q8mi94	tupaia tana
347	3	8.8	31	6	Q9GLD6	Q9gld6	sus scrofa
348	3	8.8	31	6	Q8MIH5	Q8mih5	canis famil
349	3	8.8	31	6	O77625	O77625	bos taurus
350	3	8.8	31	6	Q8MIC3	Q8mic3	ochotona pr
351	3	8.8	31	6	Q95LC0	Q95lc0	sus scrofa
352	3	8.8	31	6	Q9N1C8	Q9n1c8	ovis aries
353	3	8.8	31	6	Q8MIC9	Q8mic9	nycticebus
354	3	8.8	31	6	Q9GKL4	Q9gkl4	canis famil
355	3	8.8	31	6	Q8MIG4	Q8mig4	cynocephalu
356	3	8.8	31	6	Q9XSB9	Q9xsb9	ateles belz
357	3	8.8	31	7	Q29868	Q29868	homo sapien
358	3	8.8	31	8	Q9MNM2	Q9mnm2	bufo americ
359	3	8.8	31	8	Q9MS59	Q9ms59	euglena san
360	3	8.8	31	8	O80011	O80011	enallagma a
361	3	8.8	31	8	Q9MS62	Q9ms62	euglena myx
362	3	8.8	31	8	Q34922	Q34922	limulus pol
363	3	8.8	31	8	Q8WEJ4	Q8wej4	gnetum gnem
364	3	8.8	31	8	Q9MS74	Q9ms74	euglena ana
365	3	8.8	31	8	Q9MS68	Q9ms68	euglena des
366	3	8.8	31	8	Q8M9Y3	Q8m9y3	chaetosphae
367	3	8.8	31	8	Q9MS53	Q9ms53	euglena vir
368	3	8.8	31	8	Q9MNL2	Q9mnl2	torrentophr
369	3	8.8	31	8	Q9MS56	Q9ms56	euglena ste
370	3	8.8	31	8	Q9MS78	Q9ms78	phacus acum
371	3	8.8	31	8	Q9MNL3	Q9mnl3	torrentophr
372	3	8.8	31	9	Q38499	Q38499	bacterioph
373	3	8.8	31	10	Q9XIT0	Q9xit0	glycine max
374	3	8.8	31	10	Q8LKB4	Q8lkb4	musa acumin
375	3	8.8	31	11	Q8K1W2	Q8k1w2	cavia porce
376	3	8.8	31	11	Q9QXB6	Q9qxb6	mus musculu
377	3	8.8	31	11	Q99KK6	Q99kk6	mus musculu
378	3	8.8	31	11	Q8K1P4	Q8k1p4	sciurus vul
379	3	8.8	31	11	Q8CGM7	Q8cgm7	mus musculu
380	3	8.8	31	12	Q919E5	Q919e5	human papil
381	3	8.8	31	12	Q919E4	Q919e4	human papil
382	3	8.8	31	12	O56713	O56713	hepatitis c
383	3	8.8	31	12	Q919F7	Q919f7	human papil
384	3	8.8	31	12	Q919E6	Q919e6	human papil
385	3	8.8	31	12	O56692	O56692	hepatitis c
386	3	8.8	31	12	Q919F3	Q919f3	human papil
387	3	8.8	31	12	O56707	O56707	hepatitis c
388	3	8.8	31	12	O56687	O56687	hepatitis c
389	3	8.8	31	12	Q919F8	Q919f8	human papil
390	3	8.8	31	12	O56691	O56691	hepatitis c
391	3	8.8	31	12	Q919E1	Q919e1	human papil
392	3	8.8	31	12	O56701	O56701	hepatitis c
393	3	8.8	31	12	O56694	O56694	hepatitis c
394	3	8.8	31	12	Q919D9	Q919d9	human papil
395	3	8.8	31	12	Q919F6	Q919f6	human papil
396	3	8.8	31	12	Q919E3	Q919e3	human papil
397	3	8.8	31	12	O56712	O56712	hepatitis c
398	3	8.8	31	12	Q919E8	Q919e8	human papil
399	3	8.8	31	12	O56710	O56710	hepatitis c

400	3	8.8	31	12	056688	056688 hepatitis c
401	3	8.8	31	12	056696	056696 hepatitis c
402	3	8.8	31	12	056695	056695 hepatitis c
403	3	8.8	31	12	056698	056698 hepatitis c
404	3	8.8	31	12	056702	056702 hepatitis c
405	3	8.8	31	12	056703	056703 hepatitis c
406	3	8.8	31	12	056697	056697 hepatitis c
407	3	8.8	31	12	Q919F0	Q919f0 human papil
408	3	8.8	31	12	056709	056709 hepatitis c
409	3	8.8	31	12	Q919F4	Q919f4 human papil
410	3	8.8	31	12	056689	056689 hepatitis c
411	3	8.8	31	12	Q919F2	Q919f2 human papil
412	3	8.8	31	12	Q919F1	Q919f1 human papil
413	3	8.8	31	12	056711	056711 hepatitis c
414	3	8.8	31	12	Q919E2	Q919e2 human papil
415	3	8.8	31	12	Q919D8	Q919d8 human papil
416	3	8.8	31	12	056686	056686 hepatitis c
417	3	8.8	31	12	Q9WMX5	Q9wmx5 human echov
418	3	8.8	31	12	056690	056690 hepatitis c
419	3	8.8	31	12	Q919E9	Q919e9 human papil
420	3	8.8	31	12	056706	056706 hepatitis c
421	3	8.8	31	12	056700	056700 hepatitis c
422	3	8.8	31	12	056704	056704 hepatitis c
423	3	8.8	31	12	Q919D7	Q919d7 human papil
424	3	8.8	31	12	Q919F5	Q919f5 human papil
425	3	8.8	31	12	056693	056693 hepatitis c
426	3	8.8	31	12	056685	056685 hepatitis c
427	3	8.8	31	12	056708	056708 hepatitis c
428	3	8.8	31	12	Q919E0	Q919e0 human papil
429	3	8.8	31	12	056705	056705 hepatitis c
430	3	8.8	31	12	Q919E7	Q919e7 human papil
431	3	8.8	31	12	Q914M9	Q914m9 sulfolobus
432	3	8.8	31	12	056699	056699 hepatitis c
433	3	8.8	31	13	042540	042540 brachydanio
434	3	8.8	31	13	Q91763	Q91763 xenopus lae
435	3	8.8	31	13	Q9PSU1	Q9psul xenopus lae
436	3	8.8	31	13	Q91816	Q91816 xenopus lae
437	3	8.8	31	15	Q83937	Q83937 ovine lenti
438	3	8.8	31	16	025108	025108 helicobacte
439	3	8.8	31	16	050709	050709 borrelia bu
440	3	8.8	31	16	050818	050818 borrelia bu
441	3	8.8	31	16	050858	050858 borrelia bu
442	3	8.8	31	16	051007	051007 borrelia bu
443	3	8.8	31	16	Q9PGF2	Q9pgf2 xylella fas
444	3	8.8	31	16	Q9PAW4	Q9paw4 xylella fas
445	3	8.8	31	16	Q9KVF3	Q9kvf3 vibrio chol
446	3	8.8	31	16	Q9K7A8	Q9k7a8 bacillus ha
447	3	8.8	31	16	Q97SZ9	Q97sz9 streptococc
448	3	8.8	31	16	Q97SW8	Q97sw8 streptococc
449	3	8.8	31	16	Q97QJ4	Q97qj4 streptococc
450	3	8.8	31	16	Q97QB7	Q97qb7 streptococc
451	3	8.8	31	16	Q97CV6	Q97cv6 streptococc
452	3	8.8	31	16	Q9K2A0	Q9k2a0 chlamydia p
453	3	8.8	31	16	Q9K236	Q9k236 chlamydia p
454	3	8.8	31	16	Q8P9W1	Q8p9w1 xanthomonas
455	3	8.8	31	16	Q8KEV8	Q8kev8 chlorobium
456	3	8.8	31	16	Q8KCQ0	Q8kcq0 chlorobium

457	3	8.8	31	16	Q8KBJ8	Q8kbj8 chlorobium
458	3	8.8	31	16	Q8EIW8	Q8eiw8 shewanella
459	3	8.8	31	16	Q8EI77	Q8ei77 shewanella
460	3	8.8	31	16	Q8E9Y5	Q8e9y5 shewanella
461	3	8.8	31	16	Q8E8G1	Q8e8g1 shewanella
462	3	8.8	31	16	Q8CTW3	Q8ctw3 staphylococ
463	3	8.8	31	16	Q8CTA2	Q8cta2 staphylococ
464	3	8.8	32	2	Q9AJ41	Q9aj41 buchnera ap
465	3	8.8	32	2	Q00491	Q00491 streptomyce
466	3	8.8	32	2	Q49249	Q49249 mycoplasma
467	3	8.8	32	2	Q44499	Q44499 anabaena va
468	3	8.8	32	2	Q9S629	Q9s629 prochloroco
469	3	8.8	32	2	Q8KYN3	Q8kyn3 bacillus an
470	3	8.8	32	2	Q44509	Q44509 azotobacter
471	3	8.8	32	2	Q45534	Q45534 bacillus su
472	3	8.8	32	2	Q8VN21	Q8vn21 kluyvera ci
473	3	8.8	32	2	Q9R5Q7	Q9r5q7 aeromonas h
474	3	8.8	32	2	Q8KYM4	Q8kym4 bacillus an
475	3	8.8	32	2	O32493	O32493 bacteroides
476	3	8.8	32	2	Q8VNT6	Q8vnt6 enterobacte
477	3	8.8	32	2	Q9L373	Q9l373 rhizobium l
478	3	8.8	32	2	Q8GF58	Q8gf58 zymomonas m
479	3	8.8	32	3	Q01058	Q01058 kluyveromyc
480	3	8.8	32	3	Q8TGT3	Q8tgt3 saccharomyc
481	3	8.8	32	4	Q12900	Q12900 homo sapien
482	3	8.8	32	4	Q9UEB0	Q9ueb0 homo sapien
483	3	8.8	32	4	Q8TC25	Q8tc25 homo sapien
484	3	8.8	32	4	Q96GM7	Q96gm7 homo sapien
485	3	8.8	32	4	Q9HAX8	Q9hax8 homo sapien
486	3	8.8	32	4	Q8TBQ3	Q8tbq3 homo sapien
487	3	8.8	32	4	Q96I20	Q96i20 homo sapien
488	3	8.8	32	4	Q9UN69	Q9un69 homo sapien
489	3	8.8	32	4	Q9UQV1	Q9uqv1 homo sapien
490	3	8.8	32	5	Q9GPD9	Q9gpd9 drosophila
491	3	8.8	32	5	Q8T382	Q8t382 leishmania
492	3	8.8	32	5	O96634	O96634 trypanosoma
493	3	8.8	32	5	Q9TWR8	Q9twr8 procambarus
494	3	8.8	32	5	O18606	O18606 branchiosto
495	3	8.8	32	5	Q8T757	Q8t757 branchiosto
496	3	8.8	32	6	Q9TR67	Q9tr67 sus scrofa
497	3	8.8	32	6	Q9TR69	Q9tr69 sus scrofa
498	3	8.8	32	6	Q9TSE6	Q9tse6 oryctolagus
499	3	8.8	32	6	Q8MJ91	Q8mj91 macaca mula
500	3	8.8	32	7	Q8SNF1	Q8snf1 gallinago m
501	3	8.8	32	7	O19722	O19722 homo sapien
502	3	8.8	32	8	Q36494	Q36494 farfantepen
503	3	8.8	32	8	Q8SL89	Q8sl89 euglena ste
504	3	8.8	32	8	Q9GF95	Q9gf95 cercidiphyl
505	3	8.8	32	8	Q31736	Q31736 beta vulgar
506	3	8.8	32	8	Q8SL87	Q8sl87 euglena vir
507	3	8.8	32	8	Q31735	Q31735 beta vulgar
508	3	8.8	32	8	Q9MNM0	Q9mnm0 bufo andrew
509	3	8.8	32	8	Q9MNL0	Q9mnl0 bufo danate
510	3	8.8	32	8	Q951Q4	Q951q4 renilla ren
511	3	8.8	32	8	Q9GF72	Q9gf72 saururus ce
512	3	8.8	32	9	Q9MBU5	Q9mbu5 chlamydia p
513	3	8.8	32	10	Q8S527	Q8s527 ipomoea bat

514	3	8.8	32	10	Q8RXQ5	Q8rxq5 arabidopsis
515	3	8.8	32	10	Q40727	Q40727 oryza sativ
516	3	8.8	32	11	Q9JIU1	Q9jjiu1 rattus norv
517	3	8.8	32	11	Q9R0E3	Q9r0e3 mus musculu
518	3	8.8	32	11	Q9QWM2	Q9qwm2 mus musculu
519	3	8.8	32	11	Q9QWB2	Q9qwb2 rattus sp.
520	3	8.8	32	11	Q9QXX1	Q9qxx1 mus musculu
521	3	8.8	32	11	Q8C2N8	Q8c2n8 mus musculu
522	3	8.8	32	11	Q8BS12	Q8bs12 mus musculu
523	3	8.8	32	12	Q9PXV2	Q9pxv2 hepatitis b
524	3	8.8	32	12	Q9WNI5	Q9wni5 tt virus. o
525	3	8.8	32	12	Q914F9	Q914f9 sulfolobus
526	3	8.8	32	12	Q8QYT4	Q8qyt4 grapevine v
527	3	8.8	32	12	Q8QYT7	Q8qyt7 grapevine v
528	3	8.8	32	12	Q8QYU0	Q8qyu0 grapevine v
529	3	8.8	32	12	Q9Q934	Q9q934 shope fibro
530	3	8.8	32	13	Q8QG73	Q8qg73 oncorhynch
531	3	8.8	32	13	Q8QG72	Q8qg72 salmo salar
532	3	8.8	32	13	Q8QG71	Q8qg71 oncorhynch
533	3	8.8	32	13	Q9PS21	Q9ps21 carassius a
534	3	8.8	32	13	Q8QG84	Q8qg84 oncorhynch
535	3	8.8	32	13	Q8QG83	Q8qg83 oncorhynch
536	3	8.8	32	13	Q8QG82	Q8qg82 oncorhynch
537	3	8.8	32	13	Q8QG70	Q8qg70 salvelinus
538	3	8.8	32	13	P82780	P82780 rana catesb
539	3	8.8	32	13	Q9W7P3	Q9w7p3 morone saxa
540	3	8.8	32	13	Q9W7P2	Q9w7p2 morone saxa
541	3	8.8	32	16	O50706	O50706 borrelia bu
542	3	8.8	32	16	O50851	O50851 borrelia bu
543	3	8.8	32	16	O50865	O50865 borrelia bu
544	3	8.8	32	16	O51003	O51003 borrelia bu
545	3	8.8	32	16	Q9PGT0	Q9pgt0 xylella fas
546	3	8.8	32	16	Q9KVF7	Q9kvf7 vibrio chol
547	3	8.8	32	16	Q9KTV2	Q9ktv2 vibrio chol
548	3	8.8	32	16	Q9KPN9	Q9kpn9 vibrio chol
549	3	8.8	32	16	Q9KLF0	Q9klf0 vibrio chol
550	3	8.8	32	16	Q9K7B0	Q9k7b0 bacillus ha
551	3	8.8	32	16	Q9A2H0	Q9a2h0 caulobacter
552	3	8.8	32	16	Q98AB6	Q98ab6 rhizobium l
553	3	8.8	32	16	Q8X3V6	Q8x3v6 escherichia
554	3	8.8	32	16	Q8KG49	Q8kg49 chlorobium
555	3	8.8	32	16	Q8KEZ9	Q8kez9 chlorobium
556	3	8.8	32	16	Q8KCV3	Q8kcv3 chlorobium
557	3	8.8	32	16	Q9K4G0	Q9k4g0 streptomyce
558	3	8.8	32	16	Q8EJ44	Q8ej44 shewanella
559	3	8.8	32	16	Q8EAD5	Q8ead5 shewanella
560	3	8.8	32	16	Q8CU60	Q8cu60 staphylococ
561	3	8.8	32	16	Q8CTR7	Q8ctr7 staphylococ
562	3	8.8	32	16	Q8CRE7	Q8cre7 staphylococ
563	3	8.8	32	17	Q8ZZF7	Q8zzf7 pyrobaculum
564	3	8.8	33	1	Q9UWL4	Q9uwl4 methanopyru
565	3	8.8	33	2	Q8KH96	Q8kh96 pseudomonas
566	3	8.8	33	2	Q9S624	Q9s624 prochloroco
567	3	8.8	33	2	Q9R2M3	Q9r2m3 prochloroco
568	3	8.8	33	2	Q9X3M5	Q9x3m5 prochloroco
569	3	8.8	33	2	Q9S651	Q9s651 streptococc
570	3	8.8	33	2	Q9K533	Q9k533 listeria mo

571	3	8.8	33	2	Q9K370	Q9k370 rhizobium l
572	3	8.8	33	2	Q9F2C4	Q9f2c4 salmonella
573	3	8.8	33	2	Q9S3N5	Q9s3n5 bacillus ce
574	3	8.8	33	2	Q8KQ80	Q8kq80 vibrio chol
575	3	8.8	33	2	Q56414	Q56414 escherichia
576	3	8.8	33	2	Q9S622	Q9s622 prochloroco
577	3	8.8	33	2	Q9K2V1	Q9k2v1 rhizobium l
578	3	8.8	33	2	Q9F1F4	Q9f1f4 enterococcu
579	3	8.8	33	2	Q9KI23	Q9ki23 helicobacte
580	3	8.8	33	2	Q8GQU2	Q8gqu2 leptospira
581	3	8.8	33	3	Q8TGR1	Q8tgr1 saccharomyc
582	3	8.8	33	4	Q99950	Q99950 homo sapien
583	3	8.8	33	4	Q9UP36	Q9up36 homo sapien
584	3	8.8	33	4	Q15285	Q15285 homo sapien
585	3	8.8	33	4	Q9UDI1	Q9udi1 homo sapien
586	3	8.8	33	4	Q9P1T8	Q9plt8 homo sapien
587	3	8.8	33	4	Q9BV16	Q9bv16 homo sapien
588	3	8.8	33	4	Q92668	Q92668 homo sapien
589	3	8.8	33	5	Q9GTB2	Q9gtb2 eimeria ten
590	3	8.8	33	5	Q9GT93	Q9gt93 cryptospori
591	3	8.8	33	5	Q26673	Q26673 tethya aura
592	3	8.8	33	5	Q26672	Q26672 tethya aura
593	3	8.8	33	5	Q9GTC2	Q9gtc2 plasmodium
594	3	8.8	33	5	Q27637	Q27637 drosophila
595	3	8.8	33	5	Q9GTB3	Q9gtb3 eimeria ten
596	3	8.8	33	5	Q9GTA6	Q9gta6 sarcocystis
597	3	8.8	33	5	Q9GTA1	Q9gta1 babesia bov
598	3	8.8	33	5	Q17293	Q17293 cancer ante
599	3	8.8	33	5	Q27310	Q27310 paramecium
600	3	8.8	33	5	Q9GTA9	Q9gta9 sarcocystis
601	3	8.8	33	5	O17147	O17147 echinococcu
602	3	8.8	33	5	Q9GT95	Q9gt95 cryptospori
603	3	8.8	33	5	Q9GTA2	Q9gta2 babesia bov
604	3	8.8	33	5	Q9VHD7	Q9vhd7 drosophila
605	3	8.8	33	6	Q28788	Q28788 papio hamad
606	3	8.8	33	6	O18916	O18916 sus scrofa
607	3	8.8	33	6	Q9TSX7	Q9tsx7 sus scrofa
608	3	8.8	33	6	Q95M05	Q95m05 bos taurus
609	3	8.8	33	7	Q8MGU2	Q8mgu2 bos taurus
610	3	8.8	33	7	Q8SNF0	Q8snf0 gallinago m
611	3	8.8	33	8	Q9BAC6	Q9bac6 euglena gra
612	3	8.8	33	8	Q8W9G0	Q8w9g0 meloidogyne
613	3	8.8	33	8	Q9BAC1	Q9bac1 euglena ste
614	3	8.8	33	8	Q9XNP3	Q9xnp3 boophilus m
615	3	8.8	33	8	O78857	O78857 phytophthor
616	3	8.8	33	8	Q9T2N1	Q9t2n1 nicotiana t
617	3	8.8	33	8	Q9BAC4	Q9bac4 euglena mut
618	3	8.8	33	8	Q8WEJ5	Q8wej5 ginkgo bilo
619	3	8.8	33	8	Q8HUH3	Q8huh3 chlamydomon
620	3	8.8	33	8	Q8HS33	Q8hs33 hydrastis c
621	3	8.8	33	9	Q38588	Q38588 bacterioph
622	3	8.8	33	9	Q38551	Q38551 bacterioph
623	3	8.8	33	10	O49775	O49775 arabidopsis
624	3	8.8	33	10	Q9S8V5	Q9s8v5 zea mays (m
625	3	8.8	33	10	Q9AYQ5	Q9ayq5 cucumis sat
626	3	8.8	33	11	Q9QVM2	Q9qvm2 mus sp. glu
627	3	8.8	33	12	O72982	O72982 hepatitis c

628	3	8.8	33	12	073068	073068	hepatitis c
629	3	8.8	33	12	Q90085	Q90085	human papil
630	3	8.8	33	12	072979	072979	hepatitis c
631	3	8.8	33	12	Q91J04	Q91j04	tt virus. o
632	3	8.8	33	12	072996	072996	hepatitis c
633	3	8.8	33	12	Q91J14	Q91j14	tt virus. o
634	3	8.8	33	12	072988	072988	hepatitis c
635	3	8.8	33	12	072992	072992	hepatitis c
636	3	8.8	33	12	Q91J12	Q91j12	tt virus. o
637	3	8.8	33	12	Q91J15	Q91j15	tt virus. o
638	3	8.8	33	12	Q91J07	Q91j07	tt virus. o
639	3	8.8	33	12	072995	072995	hepatitis c
640	3	8.8	33	12	Q91J09	Q91j09	tt virus. o
641	3	8.8	33	12	072990	072990	hepatitis c
642	3	8.8	33	12	073010	073010	hepatitis c
643	3	8.8	33	12	Q86912	Q86912	hepatitis c
644	3	8.8	33	12	Q8V5G7	Q8v5g7	hepatitis c
645	3	8.8	33	12	072981	072981	hepatitis c
646	3	8.8	33	12	Q91J08	Q91j08	tt virus. o
647	3	8.8	33	12	072997	072997	hepatitis c
648	3	8.8	33	12	073008	073008	hepatitis c
649	3	8.8	33	12	Q83963	Q83963	avian influ
650	3	8.8	33	12	072986	072986	hepatitis c
651	3	8.8	33	12	072993	072993	hepatitis c
652	3	8.8	33	12	Q91J06	Q91j06	tt virus. o
653	3	8.8	33	12	072984	072984	hepatitis c
654	3	8.8	33	12	073005	073005	hepatitis c
655	3	8.8	33	12	073067	073067	hepatitis c
656	3	8.8	33	12	072985	072985	hepatitis c
657	3	8.8	33	12	072999	072999	hepatitis c
658	3	8.8	33	12	Q91J16	Q91j16	tt virus. o
659	3	8.8	33	12	072998	072998	hepatitis c
660	3	8.8	33	12	Q91J11	Q91j11	tt virus. o
661	3	8.8	33	12	072994	072994	hepatitis c
662	3	8.8	33	12	Q8V5H0	Q8v5h0	hepatitis c
663	3	8.8	33	12	Q91J13	Q91j13	tt virus. o
664	3	8.8	33	12	Q8V5G8	Q8v5g8	hepatitis c
665	3	8.8	33	12	072983	072983	hepatitis c
666	3	8.8	33	12	073007	073007	hepatitis c
667	3	8.8	33	12	Q91J10	Q91j10	tt virus. o
668	3	8.8	33	12	072987	072987	hepatitis c
669	3	8.8	33	12	Q91J17	Q91j17	tt virus. o
670	3	8.8	33	12	Q69461	Q69461	human herpe
671	3	8.8	33	12	Q8V5G9	Q8v5g9	hepatitis c
672	3	8.8	33	12	072978	072978	hepatitis c
673	3	8.8	33	12	073009	073009	hepatitis c
674	3	8.8	33	12	073004	073004	hepatitis c
675	3	8.8	33	12	Q99138	Q99138	avian influ
676	3	8.8	33	13	P82740	P82740	rana tempor
677	3	8.8	33	13	P82236	P82236	rana tempor
678	3	8.8	33	15	Q9DZ98	Q9dz98	human immun
679	3	8.8	33	15	Q86107	Q86107	simian sarc
680	3	8.8	33	16	Q9PA23	Q9pa23	xylella fas
681	3	8.8	33	16	Q9KQP4	Q9kqp4	vibrio chol
682	3	8.8	33	16	Q9KML1	Q9kml1	vibrio chol
683	3	8.8	33	16	Q97T91	Q97t91	streptococc
684	3	8.8	33	16	Q97PC1	Q97pc1	streptococc

685	3	8.8	33	16	Q932N2	Q932n2	staphylococ
686	3	8.8	33	16	Q8ZKL2	Q8zkl2	salmonella
687	3	8.8	33	16	Q8Z1V4	Q8z1v4	salmonella
688	3	8.8	33	16	Q8XAJ9	Q8xaj9	escherichia
689	3	8.8	33	16	Q8U5M4	Q8u5m4	agrobacteri
690	3	8.8	33	16	Q8VK01	Q8vk01	mycobacteri
691	3	8.8	33	16	Q8NUL1	Q8nul1	staphylococ
692	3	8.8	33	16	Q8NT95	Q8nt95	corynebacte
693	3	8.8	33	16	Q8NLP2	Q8nlp2	corynebacte
694	3	8.8	33	16	Q8KG99	Q8kg99	chlorobium
695	3	8.8	33	16	Q8KBZ0	Q8kbz0	chlorobium
696	3	8.8	33	16	Q8G0U8	Q8g0u8	brucella su
697	3	8.8	33	16	Q8FZ67	Q8fz67	brucella su
698	3	8.8	33	16	Q8FYR6	Q8fyr6	brucella su
699	3	8.8	33	16	Q8FY86	Q8fy86	brucella su
700	3	8.8	33	16	Q8FSG0	Q8fsg0	corynebacte
701	3	8.8	33	16	Q8EJH6	Q8ejh6	shewanella
702	3	8.8	33	16	Q8EGA9	Q8ega9	shewanella
703	3	8.8	33	16	Q8EE59	Q8ee59	shewanella
704	3	8.8	33	16	Q8EE42	Q8ee42	shewanella
705	3	8.8	33	16	Q8E8W4	Q8e8w4	shewanella
706	3	8.8	33	16	Q8E1Y5	Q8ely5	streptococc
707	3	8.8	33	16	Q8CTR8	Q8ctr8	staphylococ
708	3	8.8	33	16	Q8CQY7	Q8cqy7	staphylococ
709	3	8.8	33	17	Q9HSX6	Q9hsx6	halobacteri
710	3	8.8	33	17	Q8U2X8	Q8u2x8	pyrococcus
711	3	8.8	34	2	Q54427	Q54427	spiroplasma
712	3	8.8	34	2	Q9X3L6	Q9x3l6	prochloroco
713	3	8.8	34	2	Q9R5U1	Q9r5u1	campylobact
714	3	8.8	34	2	Q44208	Q44208	pseudomonas
715	3	8.8	34	2	Q9X7J6	Q9x7j6	pseudomonas
716	3	8.8	34	2	Q8KYH2	Q8kyh2	bacillus an
717	3	8.8	34	2	O31061	O31061	butyrivibri
718	3	8.8	34	2	Q9R8A2	Q9r8a2	chlamydia t
719	3	8.8	34	2	Q9RZW6	Q9rzw6	borrelia bu
720	3	8.8	34	2	Q8GJC8	Q8gjc8	campylobact
721	3	8.8	34	2	Q8G8C9	Q8g8c9	pseudomonas
722	3	8.8	34	3	Q00377	Q00377	coccidioide
723	3	8.8	34	4	Q99910	Q99910	homo sapien
724	3	8.8	34	4	Q9H3R8	Q9h3r8	homo sapien
725	3	8.8	34	4	Q9UI64	Q9ui64	homo sapien
726	3	8.8	34	4	Q8WY57	Q8wy57	homo sapien
727	3	8.8	34	4	Q8WW51	Q8ww51	homo sapien
728	3	8.8	34	4	Q9BSP7	Q9bsp7	homo sapien
729	3	8.8	34	4	Q9H4L8	Q9h4l8	homo sapien
730	3	8.8	34	4	Q8NEQ3	Q8neq3	homo sapien
731	3	8.8	34	4	Q15251	Q15251	homo sapien
732	3	8.8	34	4	Q9NQY9	Q9nqy9	homo sapien
733	3	8.8	34	5	Q9BIP7	Q9bip7	cooperia pu
734	3	8.8	34	5	Q27821	Q27821	trichomonas
735	3	8.8	34	5	Q9GQE5	Q9gqe5	branchiosto
736	3	8.8	34	5	Q8N063	Q8n063	plasmodium
737	3	8.8	34	6	Q9TS91	Q9ts91	oryctolagus
738	3	8.8	34	6	P79429	P79429	capra hircu
739	3	8.8	34	6	Q9TRI2	Q9tri2	sus scrofa
740	3	8.8	34	6	P82908	P82908	bos taurus
741	3	8.8	34	8	O79025	O79025	enallagma v

742	3	8.8	34	8	Q9T2T7	Q9t2t7 bos taurus
743	3	8.8	34	8	Q8MCA2	Q8mca2 phaseolus a
744	3	8.8	34	8	Q8HKE1	Q8hke1 rhipicephal
745	3	8.8	34	10	Q8W2H0	Q8w2h0 paspalum no
746	3	8.8	34	10	Q8VWL0	Q8vwl0 paspalum no
747	3	8.8	34	10	Q9SCA3	Q9sca3 lycopersico
748	3	8.8	34	11	Q923Z1	Q923z1 mus musculu
749	3	8.8	34	11	Q8R557	Q8r557 mus musculu
750	3	8.8	34	11	Q9ET72	Q9et72 mus musculu
751	3	8.8	34	11	Q99KM9	Q99km9 mus musculu
752	3	8.8	34	11	Q99KX7	Q99kx7 mus musculu
753	3	8.8	34	11	Q64170	Q64170 mus sp. b-r
754	3	8.8	34	11	Q8VHL4	Q8vhl4 rattus norv
755	3	8.8	34	12	Q9DW68	Q9dw68 rat cytomeg
756	3	8.8	34	13	O42521	O42521 scyliorhinu
757	3	8.8	34	13	O13101	O13101 ambystoma m
758	3	8.8	34	13	Q8QGG2	Q8qgg2 oncorhynch
759	3	8.8	34	13	Q8QFM9	Q8qfm9 oncorhynch
760	3	8.8	34	13	O42526	O42526 scyliorhinu
761	3	8.8	34	13	Q9PRE7	Q9pre7 oryzias lat
762	3	8.8	34	13	Q8QGG1	Q8qgg1 oncorhynch
763	3	8.8	34	13	Q8QGF7	Q8qgf7 oncorhynch
764	3	8.8	34	13	Q98TM8	Q98tm8 platichthys
765	3	8.8	34	15	O40445	O40445 human immun
766	3	8.8	34	15	Q9WR32	Q9wr32 human immun
767	3	8.8	34	15	Q9W8Y1	Q9w8y1 chimpanzee
768	3	8.8	34	16	O50812	O50812 borrelia bu
769	3	8.8	34	16	O50877	O50877 borrelia bu
770	3	8.8	34	16	Q9PGH3	Q9pgh3 xylella fas
771	3	8.8	34	16	Q9PGF8	Q9pgf8 xylella fas
772	3	8.8	34	16	Q9PFA5	Q9pfa5 xylella fas
773	3	8.8	34	16	Q9PDD0	Q9pdd0 xylella fas
774	3	8.8	34	16	Q9KRA8	Q9kra8 vibrio chol
775	3	8.8	34	16	Q9KPW9	Q9kpw9 vibrio chol
776	3	8.8	34	16	Q9KM63	Q9km63 vibrio chol
777	3	8.8	34	16	Q9K7C6	Q9k7c6 bacillus ha
778	3	8.8	34	16	Q9JY24	Q9jy24 neisseria m
779	3	8.8	34	16	Q9JVP3	Q9jvp3 neisseria m
780	3	8.8	34	16	Q9JUR9	Q9jur9 neisseria m
781	3	8.8	34	16	Q97SF7	Q97sf7 streptococc
782	3	8.8	34	16	Q97PI6	Q97pi6 streptococc
783	3	8.8	34	16	Q9K2B9	Q9k2b9 chlamydia p
784	3	8.8	34	16	Q8X4V1	Q8x4v1 escherichia
785	3	8.8	34	16	Q8U5V2	Q8u5v2 agrobacteri
786	3	8.8	34	16	Q8VIY1	Q8viy1 mycobacteri
787	3	8.8	34	16	Q8RIC7	Q8ric7 fusobacteri
788	3	8.8	34	16	Q8NWX3	Q8nwx3 staphylococ
789	3	8.8	34	16	Q8NV10	Q8nv10 staphylococ
790	3	8.8	34	16	Q8KEQ8	Q8keq8 chlorobium
791	3	8.8	34	16	Q8KEL5	Q8kel5 chlorobium
792	3	8.8	34	16	Q8KDE4	Q8kde4 chlorobium
793	3	8.8	34	16	Q8F897	Q8f897 leptospira
794	3	8.8	34	16	Q8F830	Q8f830 leptospira
795	3	8.8	34	16	Q8F827	Q8f827 leptospira
796	3	8.8	34	16	Q8F5Y7	Q8f5y7 leptospira
797	3	8.8	34	16	Q8F0V9	Q8f0v9 leptospira
798	3	8.8	34	16	Q8EZR6	Q8ezr6 leptospira



799	3	8.8	34	16	Q8EZ37	Q8ez37 leptospira
800	3	8.8	34	16	Q8EYW8	Q8eyw8 leptospira
801	3	8.8	34	16	Q8EYG6	Q8eyg6 leptospira
802	3	8.8	34	16	Q8EXH6	Q8exh6 leptospira
803	3	8.8	34	16	Q8EXA8	Q8exa8 leptospira
804	3	8.8	34	16	Q8EJ65	Q8ej65 shewanella
805	3	8.8	34	16	Q8EI45	Q8ei45 shewanella
806	3	8.8	34	16	Q8EHU5	Q8ehu5 shewanella
807	3	8.8	34	16	Q8E8Y3	Q8e8y3 shewanella
808	3	8.8	34	16	Q8E8W3	Q8e8w3 shewanella
809	3	8.8	34	16	Q8E173	Q8e173 streptococc
810	3	8.8	34	16	Q8CRY3	Q8cry3 staphylococ
811	3	8.8	34	17	Q8U1I1	Q8uli1 pyrococcus
812	3	8.8	35	2	Q9R624	Q9r624 bacillus su
813	3	8.8	35	2	Q9JPG9	Q9jpg9 neisseria m
814	3	8.8	35	2	Q9R625	Q9r625 bacillus su
815	3	8.8	35	2	Q9X3D6	Q9x3d6 prochloroco
816	3	8.8	35	2	Q9R5I3	Q9r5i3 thermoanaer
817	3	8.8	35	2	Q9FCX4	Q9fcx4 clostridium
818	3	8.8	35	2	Q9XBK0	Q9xbk0 bacillus ce
819	3	8.8	35	2	Q53564	Q53564 neisseria g
820	3	8.8	35	2	Q46537	Q46537 bacteroides
821	3	8.8	35	2	Q9ZG35	Q9zg35 chlamydia t
822	3	8.8	35	2	Q9RHG5	Q9rhg5 bacillus ce
823	3	8.8	35	2	Q9R4A1	Q9r4a1 klebsiella
824	3	8.8	35	2	O30661	O30661 vibrio chol
825	3	8.8	35	2	Q9ZG68	Q9zg68 chlamydia t
826	3	8.8	35	2	Q8RKG3	Q8rkg3 clostridium
827	3	8.8	35	2	Q8RIW2	Q8riw2 clostridium
828	3	8.8	35	2	Q9R626	Q9r626 bacillus su
829	3	8.8	35	2	P81927	P81927 lactobacill
830	3	8.8	35	3	Q96UT3	Q96ut3 saccharomyc
831	3	8.8	35	4	Q9BVR9	Q9bvr9 homo sapien
832	3	8.8	35	4	Q13380	Q13380 homo sapien
833	3	8.8	35	4	Q9BS62	Q9bs62 homo sapien
834	3	8.8	35	4	Q13165	Q13165 homo sapien
835	3	8.8	35	4	Q13828	Q13828 homo sapien
836	3	8.8	35	4	Q13264	Q13264 homo sapien
837	3	8.8	35	4	Q9Y634	Q9y634 homo sapien
838	3	8.8	35	4	Q9BU09	Q9bu09 homo sapien
839	3	8.8	35	4	Q8IU77	Q8iu77 homo sapien
840	3	8.8	35	5	Q27754	Q27754 pisaster oc
841	3	8.8	35	5	Q9U780	Q9u780 boophilus a
842	3	8.8	35	5	Q26372	Q26372 tribolium c
843	3	8.8	35	5	Q9U782	Q9u782 boophilus m
844	3	8.8	35	5	Q9TVJ7	Q9tvj7 boophilus m
845	3	8.8	35	5	Q9U783	Q9u783 boophilus m
846	3	8.8	35	5	Q9U784	Q9u784 boophilus m
847	3	8.8	35	5	Q9U781	Q9u781 boophilus m
848	3	8.8	35	5	Q8IF21	Q8if21 trypanosoma
849	3	8.8	35	6	Q95N74	Q95n74 equus cabal
850	3	8.8	35	6	Q9MZA7	Q9mza7 sus scrofa
851	3	8.8	35	8	Q951Q6	Q951q6 protoptilum
852	3	8.8	35	8	Q8W7S9	Q8w7s9 colpomenia
853	3	8.8	35	8	Q9GF85	Q9gf85 ginkgo bilo
854	3	8.8	35	8	Q8W7T0	Q8w7t0 petalonia b
855	3	8.8	35	8	Q8W7S8	Q8w7s8 petalonia f

856	3	8.8	35	8	Q8WE70	Q8we70 miliaria ca
857	3	8.8	35	8	Q8W7S7	Q8w7s7 scytosiphon
858	3	8.8	35	8	Q9GF98	Q9gf98 ceratophyll
859	3	8.8	35	8	Q95766	Q95766 cerataphis
860	3	8.8	35	8	Q94P82	Q94p82 corallium r
861	3	8.8	35	8	Q8WEJ7	Q8wej7 cycas circi
862	3	8.8	35	8	Q951S7	Q951s7 anthothela
863	3	8.8	35	8	Q951R1	Q951r1 narella nut
864	3	8.8	35	8	Q951S1	Q951s1 corallium k
865	3	8.8	35	8	Q8WII3	Q8wii3 colpomenia
866	3	8.8	35	8	Q951R3	Q951r3 anthomurice
867	3	8.8	35	8	Q8WIH9	Q8wih9 scytosiphon
868	3	8.8	35	8	Q8WIH5	Q8wih5 hydroclathr
869	3	8.8	35	8	Q951S9	Q951s9 protodendro
870	3	8.8	35	8	Q8WII1	Q8wii1 scytosiphon
871	3	8.8	35	8	Q951Q9	Q951q9 narella sp.
872	3	8.8	35	8	Q951S4	Q951s4 paragorgia
873	3	8.8	35	8	Q951R5	Q951r5 corallium s
874	3	8.8	35	10	Q9SPU2	Q9spu2 arabidopsis
875	3	8.8	35	10	Q9MAB1	Q9mab1 arabidopsis
876	3	8.8	35	10	Q9ZUW2	Q9zuw2 arabidopsis
877	3	8.8	35	10	Q9S9G9	Q9s9g9 lycopersico
878	3	8.8	35	10	P92971	P92971 arabidopsis
879	3	8.8	35	10	Q9LV08	Q9lv08 arabidopsis
880	3	8.8	35	10	Q9LQ64	Q9lq64 arabidopsis
881	3	8.8	35	10	Q94IS4	Q94is4 pinus radia
882	3	8.8	35	10	Q39297	Q39297 brassica na
883	3	8.8	35	10	Q8RVJ7	Q8rvj7 populus eur
884	3	8.8	35	10	Q9FJ84	Q9fj84 arabidopsis
885	3	8.8	35	10	Q8GUX4	Q8gux4 picea maria
886	3	8.8	35	11	Q63397	Q63397 rattus norv
887	3	8.8	35	11	Q9JLA4	Q9jla4 mus musculu
888	3	8.8	35	11	Q60608	Q60608 mus musculu
889	3	8.8	35	11	Q9QV50	Q9qv50 rattus sp.
890	3	8.8	35	11	Q9QV30	Q9qv30 rattus sp.
891	3	8.8	35	11	Q922H5	Q922h5 mus musculu
892	3	8.8	35	11	Q8BK89	Q8bk89 mus musculu
893	3	8.8	35	12	Q90151	Q90151 bombyx mori
894	3	8.8	35	12	Q65380	Q65380 banana bunc
895	3	8.8	35	12	Q83333	Q83333 murine hepa
896	3	8.8	35	12	O55549	O55549 measles vir
897	3	8.8	35	12	Q8BB50	Q8bb50 human papil
898	3	8.8	35	13	Q90XB5	Q90xb5 xenopus lae
899	3	8.8	35	13	P83224	P83224 oxyuranus m
900	3	8.8	35	13	P83225	P83225 oxyuranus s
901	3	8.8	35	13	P83227	P83227 oxyuranus m
902	3	8.8	35	13	P83228	P83228 oxyuranus s
903	3	8.8	35	13	P83229	P83229 oxyuranus s
904	3	8.8	35	13	P83226	P83226 oxyuranus s
905	3	8.8	35	15	Q75981	Q75981 human immun
906	3	8.8	35	15	Q70328	Q70328 human immun
907	3	8.8	35	15	Q70380	Q70380 human immun
908	3	8.8	35	15	Q70319	Q70319 human immun
909	3	8.8	35	15	Q79465	Q79465 human immun
910	3	8.8	35	15	Q70426	Q70426 human immun
911	3	8.8	35	15	Q9J3S2	Q9j3s2 human immun
912	3	8.8	35	15	O71950	O71950 human immun

913	3	8.8	35	15	Q9IPY2	Q9ipy2	human	immun
914	3	8.8	35	15	Q80574	Q80574	human	immun
915	3	8.8	35	15	Q70425	Q70425	human	immun
916	3	8.8	35	15	Q70362	Q70362	human	immun
917	3	8.8	35	15	Q80601	Q80601	human	immun
918	3	8.8	35	15	Q8QDX6	Q8qdx6	human	immun
919	3	8.8	35	15	Q77702	Q77702	human	immun
920	3	8.8	35	15	Q9QFA0	Q9qfa0	human	immun
921	3	8.8	35	15	Q70330	Q70330	human	immun
922	3	8.8	35	15	Q77584	Q77584	human	immun
923	3	8.8	35	15	Q70317	Q70317	human	immun
924	3	8.8	35	15	Q70316	Q70316	human	immun
925	3	8.8	35	15	Q70402	Q70402	human	immun
926	3	8.8	35	15	Q9YM80	Q9ym80	human	immun
927	3	8.8	35	15	Q8QDY0	Q8qdy0	human	immun
928	3	8.8	35	15	Q75970	Q75970	human	immun
929	3	8.8	35	15	Q70409	Q70409	human	immun
930	3	8.8	35	15	Q70325	Q70325	human	immun
931	3	8.8	35	15	Q9YM17	Q9ym17	human	immun
932	3	8.8	35	15	Q79468	Q79468	human	immun
933	3	8.8	35	15	Q9YM96	Q9ym96	human	immun
934	3	8.8	35	15	Q70363	Q70363	human	immun
935	3	8.8	35	15	Q70321	Q70321	human	immun
936	3	8.8	35	15	Q9YM22	Q9ym22	human	immun
937	3	8.8	35	15	Q75990	Q75990	human	immun
938	3	8.8	35	15	Q70323	Q70323	human	immun
939	3	8.8	35	15	Q75989	Q75989	human	immun
940	3	8.8	35	15	Q70428	Q70428	human	immun
941	3	8.8	35	15	Q9YM67	Q9ym67	human	immun
942	3	8.8	35	15	Q77585	Q77585	human	immun
943	3	8.8	35	15	Q70403	Q70403	human	immun
944	3	8.8	35	15	Q70327	Q70327	human	immun
945	3	8.8	35	15	Q77250	Q77250	human	immun
946	3	8.8	35	15	Q75955	Q75955	human	immun
947	3	8.8	35	15	Q9IPY4	Q9ipy4	human	immun
948	3	8.8	35	15	Q70424	Q70424	human	immun
949	3	8.8	35	15	Q77582	Q77582	human	immun
950	3	8.8	35	16	O07593	O07593	bacillus	su
951	3	8.8	35	16	Q9KR18	Q9kr18	vibrio	chol
952	3	8.8	35	16	Q9KNU1	Q9knul	vibrio	chol
953	3	8.8	35	16	Q9JWX5	Q9jwx5	neisseria	m
954	3	8.8	35	16	Q9JV38	Q9jv38	neisseria	m
955	3	8.8	35	16	Q9A427	Q9a427	caulobacter	
956	3	8.8	35	16	Q9K241	Q9k241	chlamydia	p
957	3	8.8	35	16	Q8XZB7	Q8xzb7	ralstonia	s
958	3	8.8	35	16	Q8X4F4	Q8x4f4	escherichia	
959	3	8.8	35	16	Q8KCA6	Q8kca6	chlorobium	
960	3	8.8	35	16	Q8G2D4	Q8g2d4	brucella	su
961	3	8.8	35	16	Q8F9H5	Q8f9h5	leptospira	
962	3	8.8	35	16	Q8F8D4	Q8f8d4	leptospira	
963	3	8.8	35	16	Q8F1W8	Q8f1w8	leptospira	
964	3	8.8	35	16	Q8EYH6	Q8eyh6	leptospira	
965	3	8.8	35	16	Q8EGT2	Q8egt2	shewanella	
966	3	8.8	35	16	Q8EGC0	Q8egc0	shewanella	
967	3	8.8	35	16	Q8EG97	Q8eg97	shewanella	
968	3	8.8	35	16	Q8EEP3	Q8eep3	shewanella	
969	3	8.8	35	16	Q8E9Z1	Q8e9z1	shewanella	

970	3	8.8	35	16	Q8DUY1	Q8duy1 streptococc
971	3	8.8	35	17	Q9HMP1	Q9hmp1 halobacteri
972	3	8.8	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
973	3	8.8	36	2	O06954	O06954 salmonella
974	3	8.8	36	2	Q8VTS7	Q8vts7 listeria in
975	3	8.8	36	2	Q9ZG79	Q9zg79 chlamydia t
976	3	8.8	36	2	Q9RHE3	Q9rhe3 pediococcus
977	3	8.8	36	2	Q8VTS5	Q8vts5 listeria we
978	3	8.8	36	2	Q44437	Q44437 agrobacteri
979	3	8.8	36	2	Q9LB55	Q9lb55 helicobacte
980	3	8.8	36	2	Q48507	Q48507 lactococcus
981	3	8.8	36	2	Q99094	Q99094 salmonella
982	3	8.8	36	2	Q9S635	Q9s635 prochloroco
983	3	8.8	36	2	Q8VTR8	Q8vtr8 listeria iv
984	3	8.8	36	2	Q8VTS0	Q8vts0 listeria mo
985	3	8.8	36	2	Q8KYW1	Q8kyw1 uncultured
986	3	8.8	36	2	Q9R4X9	Q9r4x9 azotobacter
987	3	8.8	36	2	Q9R5L0	Q9r5l0 sarcina ven
988	3	8.8	36	2	Q9X3G2	Q9x3g2 prochloroco
989	3	8.8	36	2	O86086	O86086 shewanella
990	3	8.8	36	2	Q9R536	Q9r536 sphingomona
991	3	8.8	36	2	Q8GRH1	Q8grh1 pectobacter
992	3	8.8	36	3	Q96W36	Q96w36 ophiostoma
993	3	8.8	36	4	Q9UNV7	Q9unv7 homo sapien
994	3	8.8	36	4	Q9P1E9	Q9ple9 homo sapien
995	3	8.8	36	4	Q9UPB7	Q9upb7 homo sapien
996	3	8.8	36	4	Q9UML4	Q9uml4 homo sapien
997	3	8.8	36	4	Q8NE47	Q8ne47 homo sapien
998	3	8.8	36	5	Q9GSY9	Q9gsy9 carcinus ma
999	3	8.8	36	5	Q9NGN1	Q9ngn1 strongyloce
1000	3	8.8	36	5	Q27730	Q27730 plasmodium

# ALIGNMENTS

## RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.  
AC Q91Y90;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Parathyroid hormone (Fragment).  
GN PTH.  
OS Peromyscus maniculatus (Deer mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
OC Peromyscus.  
OX NCBI\_TaxID=10042;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Prince K.L., Dewey M.J.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF382953; AAK63072.1; -.  
DR InterPro; IPR001415; Parathyrd\_hrm.  
DR InterPro; IPR003625; Pthyrhorm\_sub.

DR Pfam; PF01279; Parathyroid; 1.  
DR ProDom; PD010687; Pthyrhorm\_sub; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
FT NON\_TER 1 1  
FT NON\_TER 31 31  
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 41.2%; Score 14; DB 11; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15  
|||  
Db 14 VSEIQLMHNLGKHL 27

#### RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.  
AC Q91Y91;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Parathyroid hormone (Fragment).  
GN PTH.  
OS Peromyscus polionotus (Oldfield mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
OC Peromyscus.  
OX NCBI\_TaxID=42413;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Prince K.L., Dewey M.J.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF382952; AAK63071.1; -.  
DR InterPro; IPR001415; Parathyrd\_hrm.  
DR InterPro; IPR003625; Pthyrhorm\_sub.  
DR Pfam; PF01279; Parathyroid; 1.  
DR ProDom; PD010687; Pthyrhorm\_sub; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
FT NON\_TER 1 1  
FT NON\_TER 31 31  
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 41.2%; Score 14; DB 11; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15  
|||  
Db 14 VSEIQLMHNLGKHL 27

#### RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.  
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Antigen B/1 (Fragment).  
 GN AGB/1.  
 OS Echinococcus vogeli.  
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 OC Cyclophyllidea; Taeniidae; Echinococcus.  
 OX NCBI\_TaxID=6213;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94359533; PubMed=8078520;  
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;  
 RT "Sequence heterogeneity of the echinococcal antigen B.";  
 RL Mol. Biochem. Parasitol. 64:171-175(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Haag K.L., Zaha A., Gottstein B.;  
 RT "E. vogeli AgB/1 coding sequence.";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF024665; AAB81611.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 34 34  
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 14.7%; Score 5; DB 5; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28  
 |||||  
 Db 15 LRKKL 19

#### RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.  
 AC Q97K50;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Transcriptional regulator, AcrR family.  
 GN CAC1071.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=11466286;  
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).  
DR EMBL; AE007622; AAK79045.1; -.  
KW Complete proteome.  
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 14.7%; Score 5; DB 16; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5  
|||||  
Db 30 SVSEI 34

#### RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.  
AC Q9HR65;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Vng0840h.  
GN VNG0840H.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
RT "Genome sequence of Halobacterium species NRC-1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AE005025; AAG19293.1; -.  
KW Complete proteome.  
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 14.7%; Score 5; DB 17; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28  
|||||  
Db 26 LRKKL 30

#### RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.  
AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Translin.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Body;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK011220; BAC25325.1; -.  
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 14.7%; Score 5; DB 11; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5  
 |||||  
 Db 2 SVSEI 6

# RESULT 7

Q97RG6

ID Q97RG6 PRELIMINARY; PRT; 35 AA.  
 AC Q97RG6;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical protein SP0853.  
 GN SP0853.  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TIGR4;  
 RX MEDLINE=21357209; PubMed=11463916;  
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,  
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,  
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,  
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,  
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,  
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,  
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,  
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;  
 RT "Complete genome sequence of a virulent isolate of Streptococcus  
 RT pneumoniae."  
 RL Science 293:498-506(2001).



DR EMBL; AE007391; AAK74982.1; -.  
DR TIGR; SP0853; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;

Query Match 14.7%; Score 5; DB 16; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30  
|||  
Db 30 KKLQD 34

#### RESULT 8

O24285

ID O24285 PRELIMINARY; PRT; 28 AA.  
AC O24285;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE LFY protein (Fragment).  
GN LFY.  
OS Pinus radiata (Monterey pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=3347;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Vegetative;  
RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;  
RT "Partial characterization of Pinus radiata meristem identity homolog  
RT gene (LFY).";  
RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; U66725; AAB06792.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 28 28  
SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
|||  
Db 15 LRKK 18

#### RESULT 9

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.  
AC Q8GZQ8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE SNF-1 related kinase (Fragment).  
GN BKIN12.

OS *Hordeum vulgare* var. *distichum* (Two-rowed barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; *Hordeum*.  
 OX NCBI\_TaxID=112509;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Igri;  
 RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;  
 RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF448389; AAN76447.1; -.  
 KW Kinase.  
 FT NON\_TER 28 28  
 SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13  
 ||||  
 Db 18 NLGK 21

# RESULT 10

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.  
 AC Q49148;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE PQQ biosynthesis polypeptide.  
 GN PQQD.  
 OS *Methylobacterium extorquens*.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Methylobacteriaceae; *Methylobacterium*.  
 OX NCBI\_TaxID=408;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AM1;  
 RX MEDLINE=94179111; PubMed=8132470;  
 RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,  
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;  
 RT "Isolation, phenotypic characterization, and complementation analysis  
 RT of mutants of *Methylobacterium extorquens* AM1 unable to synthesize  
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.";  
 RL J. Bacteriol. 176:1746-1755(1994).  
 DR EMBL; L25889; AAA17878.1; -.  
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 11.8%; Score 4; DB 2; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5  
 ||||

Db 8 VSEI 11

RESULT 11

Q9UCL2

ID Q9UCL2 PRELIMINARY; PRT; 29 AA.  
AC Q9UCL2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Renal intestinal-type alkaline phosphatase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93092315; PubMed=1458595;  
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,  
RA Hirano K.;  
RT "Chemical nature of intestinal-type alkaline phosphatase in human  
RT kidney.";  
RL Clin. Chem. 38:2539-2542(1992).  
DR InterPro; IPR001952; Alk\_phosphatase.  
DR ProDom; PD001868; Alk\_phosphatase; 1.  
SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BEEAD8D0 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 29;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 23 KKLQ 26

RESULT 12

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.  
AC Q96PP3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).  
GN SPINK5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,  
RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,  
RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,  
RA Uitto J., Hovnanian A., Richard G.;  
RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with  
RT Netherton syndrome - Implications for mutation detection and first

RT case of prenatal diagnosis.";  
 RL J. Invest. Dermatol. 0:0-0(2001).  
 DR EMBL; AF295783; AAK97140.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 29 29  
 SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 11.8%; Score 4; DB 4; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLGK 13  
 ||||  
 Db 14 NLGK 17

#### RESULT 13

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.  
 AC Q25603;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Tubulin.  
 OS Onchocerca volvulus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Onchocerca.  
 OX NCBI\_TaxID=6282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chandrashekar R., Curtis K.C., Weil G.J.;  
 RT "Onchocerca volvulus cDNA clone."  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U15095; AAA50364.1; -.  
 SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5  
 ||||  
 Db 4 VSEI 7

#### RESULT 14

Q9TI61

ID Q9TI61 PRELIMINARY; PRT; 29 AA.  
 AC Q9TI61;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Photosystem Q(B) protein (Fragment).  
 GN PSBA.  
 OS Allosyncarpia ternata.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II, Myrtales; Myrtaceae; Allosyncarpia.  
 OX NCBI\_TaxID=34307;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Udovicic F., Ladiges P.Y.;  
 RT "Informativeness of nuclear and chloroplast DNA regions and the  
 RT phylogeny of the eucalypts and related genera (Myrtaceae).";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF190370; AAF15265.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 29 AA; 3501 MW; 977D8E6E67E1D833 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VHNF 34  
 ||||  
 Db 7 VHNF 10

# RESULT 15

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.  
 AC O13043;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Whn transcription factor (Fragment).  
 GN WHN.  
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268658; PubMed=9108066;  
 RA Schlake T., Schorpp M., Nehls M., Boehm T.;  
 RT "The nude gene encodes a sequence-specific DNA binding protein with  
 RT homologs in organisms that lack an anticipatory immune system.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).  
 DR EMBL; Y11539; CAA72302.1; -.  
 DR InterPro; IPR001766; TF\_Fork\_head.  
 DR Pfam; PF00250; Fork\_head; 1.  
 DR ProDom; PD000425; TF\_Fork\_head; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 29 29  
 SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5

||||  
Db 17 VSEI 20

RESULT 16

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.  
AC Q9JMV3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Luciferase alpha-subunit (Fragment).  
GN LUXA.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HB101;  
RA Lotz W., Bauer T.;  
RT "luxAB/kan-cassette for site-directed insertion mutagenesis and  
RT bacterial transcription studies.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HB101;  
RA Olsson O., Koncz C., Szalay A.;  
RT "The use of luxA gene of the bacterial luciferase operon as a reporter  
RT gene.";  
RL Mol. Gen. Genet. 215:1-9(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HB101;  
RX MEDLINE=92114868; PubMed=1685011;  
RA Escher A., O'Kane D.J., Szalay A.;  
RT "The beta subunit polypeptide of Vibrio harveyi luciferase determines  
RT light emission at 42 degrees C.";  
RL Mol. Gen. Genet. 230:385-393(1991).  
DR EMBL; AJ249443; CAB96206.1; -.  
DR HSSP; P07740; 1LUC.  
DR InterPro; IPR002103; Bac\_luciferase.  
DR Pfam; PF00296; bac\_luciferase; 1.  
FT NON\_TER 30 30  
SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 11.8%; Score 4; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLGK 13  
||||  
Db 26 NLGK 29

RESULT 17

Q9UBV5

ID Q9UBV5 PRELIMINARY; PRT; 30 AA.  
AC Q9UBV5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Intestinal alkaline phosphatase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93092315; PubMed=1458595;  
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,  
RA Hirano K.;  
RT "Chemical nature of intestinal-type alkaline phosphatase in human  
RT kidney.";  
RL Clin. Chem. 38:2539-2542(1992).  
DR InterPro; IPR001952; Alk\_phosphatase.  
DR ProDom; PD001868; Alk\_phosphatase; 1.  
SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BEB9BDE6 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 24 KKLQ 27

RESULT 18  
Q8DZP7

ID Q8DZP7 PRELIMINARY; PRT; 30 AA.  
AC Q8DZP7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN SAG1053.  
OS Streptococcus agalactiae (serotype V).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=216466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2603 V/R / Serotype V;  
RX MEDLINE=22222988; PubMed=12200547;  
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,  
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,  
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,  
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,  
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,  
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,  
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,  
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,  
RA Fraser C.M.;

RT "Complete genome sequence and comparative genomic analysis of an  
RT emerging human pathogen, serotype V Streptococcus agalactiae.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).  
DR EMBL; AE014240; AAM99934.1; -.  
DR TIGR; SAG1053; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 23 KKLQ 26

RESULT 19

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.  
AC Q55314;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Urf2 protein (Fragment).  
GN URF2.  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96085144; PubMed=8521845;  
RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;  
RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate  
RT dehydrogenase genes from the thermophilic archaeon Sulfolobus  
RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and  
RT expression on Escherichia coli.";  
RL Eur. J. Biochem. 233:800-808(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94082761; PubMed=8259927;  
RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;  
RT "Nucleotide sequence and molecular evolution of the gene coding for  
RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic  
RT archaeobacterium Sulfolobus solfataricus.";  
RL Biochem. Genet. 31:241-251(1993).  
DR EMBL; X80178; CAA56461.1; -.  
FT NON\_TER 31 31  
SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26  
|||



Db 11 WLRK 14

RESULT 20

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.  
AC Q8NEI8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC030993; AAH30993.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5  
|||  
Db 18 VSEI 21

RESULT 21

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.  
AC Q9MS77;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Photosystem I protein M.  
GN PSAM.  
OS Phacus acuminata.  
OG Chloroplast.  
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.  
OX NCBI\_TaxID=130316;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21080550; PubMed=11212923;  
RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;  
RT "Comparison of psbK operon organization and group III intron content  
RT in chloroplast genomes of 12 Euglenoid species.";  
RL Mol. Gen. Genet. 264:682-690(2001).  
DR EMBL; AF241276; AAF82438.1; -.  
KW Chloroplast.  
SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13  
|||  
Db 24 NLGK 27

RESULT 22

O50669

ID O50669 PRELIMINARY; PRT; 31 AA.  
AC O50669;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein BBH11.  
GN BBH11.  
OS *Borrelia burgdorferi* (Lyme disease spirochete).  
OG Plasmid lp28-3.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35210 / B31;  
RX MEDLINE=98065943; PubMed=9403685;  
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,  
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,  
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,  
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,  
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,  
RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,  
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,  
RA Smith H.O., Venter J.C.;  
RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia*  
RT *burgdorferi*."  
RL Nature 390:580-586(1997).  
DR EMBL; AE000784; AAC66002.1; -.  
DR TIGR; BBH11; -.  
KW Hypothetical protein; Plasmid; Complete proteome.  
SQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 11.8%; Score 4; DB 16; Length 31;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 26 KKLQ 29

RESULT 23

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.  
AC Q9QZQ2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Neurotensin receptor (Fragment).  
 GN NTSR OR NTR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=99445567; PubMed=10514493;  
 RA Tavares D., Tully K., Dobner P.R.;  
 RT "Sequences required for induction of neurotensin receptor gene  
 RT expression during neuronal differentiation of N1E-115 neuroblastoma  
 RT cells.";  
 RL J. Biol. Chem. 274:30066-30079(1999).  
 DR EMBL; AF172326; AAD51806.1; -.  
 DR MGD; MGI:97386; Ntsr.  
 KW Receptor.  
 FT NON\_TER 32 32  
 SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 11.8%; Score 4; DB 11; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17  
 ||||  
 Db 2 HLNS 5

#### RESULT 24

Q9HSZ0

ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.  
 AC Q9HSZ0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Vng0019h.  
 GN VNG0019H.  
 OS Halobacterium sp. (strain NRC-1).  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 OX NCBI\_TaxID=64091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20504483; PubMed=11016950;  
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
 RT "Genome sequence of Halobacterium species NRC-1.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AE004971; AAG18659.1; -.  
KW Complete proteome.  
SQ SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64;

Query Match 11.8%; Score 4; DB 17; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30  
|||  
Db 13 KLQD 16

RESULT 25

Q95SD4

ID Q95SD4 PRELIMINARY; PRT; 33 AA.  
AC Q95SD4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE GM02640p.  
GN BCDNA:GM02640.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY060847; AAL28395.1; -.  
DR FlyBase; FBgn0047288; BcdNA:GM02640.  
SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBE4A7 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 21 KKLQ 24

RESULT 26

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.  
AC Q9PKX3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical protein TC0337.

GN TC0337.  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MoPn / Nigg;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 DR EMBL; AE002301; AAF39200.1; -.  
 DR TIGR; TC0337; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 11.8%; Score 4; DB 16; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
 ||||  
 Db 26 LRKK 29

# RESULT 27

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.  
 AC Q9ZG81;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE ATP-dependent permease (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L2 434B;  
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;  
 RT "Gene identification of Chlamydia trachomatis by random DNA  
 RT sequencing.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF087260; AAD04038.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 34 34  
 SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
|||  
Db 25 LRKK 28

RESULT 28

Q8GFK2

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.  
AC Q8GFK2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE ORF37.  
OS Staphylococcus aureus.  
OG Plasmid EDINA plasmid.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E-1;  
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;  
RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA  
RT plasmid.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AP003089; BAC54529.1; -.  
KW Plasmid.  
SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
|||  
Db 6 KKLQ 9

RESULT 29

Q8C4P4

ID Q8C4P4 PRELIMINARY; PRT; 34 AA.  
AC Q8C4P4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Zinc finger homeodomain 4 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).  
DR EMBL; AK081561; BAC38260.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;

Query Match 11.8%; Score 4; DB 11; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30  
|||  
Db 2 KLQD 5

RESULT 30

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.  
AC Q90ZJ4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Platelet-derived growth factor A chain long form (Fragment).  
GN PDGF-A.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21363439; PubMed=11470524;  
RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;  
RT "Characterization and expression of three forms of cDNA encoding  
RT chicken platelet-derived growth factor-A chain."  
RL Gene 272:181-190(2001).  
DR EMBL; AB031024; BAB62544.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28  
|||  
Db 28 RKKL 31

RESULT 31

Q98FK5

ID Q98FK5 PRELIMINARY; PRT; 34 AA.  
AC Q98FK5;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein msr3733.  
GN MSR3733.

OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003002; BAB50562.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 34 AA; 3804 MW; D6AAA82ECB590413 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30  
 ||||  
 Db 28 KLQD 31

# RESULT 32

Q8G2Q2

ID Q8G2Q2 PRELIMINARY; PRT; 34 AA.  
 AC Q8G2Q2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN BR0266.  
 OS Brucella suis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;  
 RT "The Brucella suis genome reveals fundamental similarities between  
 RT animal and plant pathogens and symbionts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
 DR EMBL; AE014339; AAN29215.1; -.  
 DR TIGR; BR0266; -.



KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 34 AA; 3781 MW; 76E820326E6CA66E CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LGKH 14

||||

Db 10 LGKH 13

#### RESULT 33

Q15421

ID Q15421 PRELIMINARY; PRT; 35 AA.

AC Q15421;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE Simian sarcoma associated virus (SSAV)-related pol region DNA  
(Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87071681; PubMed=2431542;

RA Leib-Mosch C., Brack R., Werner T., Erfle V., Hehlmann R.;

RT "Isolation of an SSAV-related endogenous sequence from Human DNA.";

RL Virology 155:666-677(1986).

DR EMBL; M14911; AAA36592.1; -.

FT NON\_TER 1 1

FT NON\_TER 35 35

SQ SEQUENCE 35 AA; 3742 MW; 2F70B02EE0BC86DF CRC64;

Query Match 11.8%; Score 4; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQDV 31

||||

Db 6 LQDV 9

#### RESULT 34

Q8V6J8

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.

AC Q8V6J8;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical 4.1 kDa protein.

OS Halovirus HF2.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.

OX NCBI\_TaxID=33771;

RN [1]

RP SEQUENCE FROM N.A.  
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyall-Smith M.L.;  
RT "Sequence and transcription of halovirus HF2.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF222060; AAL55025.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 35 AA; 4115 MW; 2652C319622E9CE4 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4  
|||  
Db 10 SVSE 13

RESULT 35

Q9KQG4

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.  
AC Q9KQG4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical protein VC2034.  
GN VC2034.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=El Tor N16961 / Serotype O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
RT cholerae.";  
RL Nature 406:477-483(2000).  
DR EMBL; AE004278; AAF95182.1; -.  
DR TIGR; VC2034; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
||||  
Db 24 KKLQ 27

RESULT 36

Q8F102

ID Q8F102 PRELIMINARY; PRT; 35 AA.  
 AC Q8F102;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN LA3339.  
 OS Leptospira interrogans.  
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
 OX NCBI\_TaxID=173;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
 RA Ren S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AE011494; AAN50536.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17  
 ||||  
 Db 3 HLNS 6

RESULT 37

Q53920

ID Q53920 PRELIMINARY; PRT; 36 AA.  
 AC Q53920;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE OrfA protein (Fragment).  
 GN ORFA.  
 OS Streptomyces chrysomallus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1899;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94341259; PubMed=8062824;  
 RA Pahl A., Keller U.;  
 RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting  
 RT of two FK506-binding domains with its gene transcriptionally coupled  
 RT to the FKBP-12 gene.";  
 RL EMBO J. 13:3472-3480(1994).  
 DR EMBL; Z34523; CAA84281.1; -.  
 DR InterPro; IPR004347; DUF245.  
 DR Pfam; PF03136; DUF245; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 36 AA; 4121 MW; EBD470AAF99A728E CRC64;

Query Match 11.8%; Score 4; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22  
|||  
Db 27 ERVE 30

RESULT 38

O68941

ID O68941 PRELIMINARY; PRT; 36 AA.  
AC O68941;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Dinitrogenase 3 beta subunit (Fragment).  
GN ANFK.  
OS Rhodospirillum rubrum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Rhodospirillaceae; Rhodospirillum.  
OX NCBI\_TaxID=1085;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Loveless T.M., Bishop P.E.;  
RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems  
RT in Diverse Diazotrophs.";  
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF058778; AAC14327.1; -.  
DR InterPro; IPR000510; Oxred\_nitrognse1.  
DR Pfam; PF00148; oxidored\_nitro; 1.  
FT NON\_TER 36 36  
SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFD437D97 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27  
|||  
Db 5 LRKK 8

RESULT 39

Q8WXW8

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.  
AC Q8WXW8;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Urea transporter JK glycoprotein (Fragment).  
GN JK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;  
 RT "Molecular Basis of the Jk(a-b-) Phenotype in Non-Finnish European  
 RT Pedigrees.";  
 RL Br. J. Haematol. 0:0-0(2001).  
 DR EMBL; AF328890; AAL37474.1; -.  
 DR InterPro; IPR004937; Urea\_transporter.  
 DR Pfam; PF03253; UT; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;  
  
 Query Match 11.8%; Score 4; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNSM 18  
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 Db 7 LNSM 10

RESULT 40

Q9SJ63

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.  
 AC Q9SJ63;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE At2g35870 protein.  
 GN AT2G35870.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 402:761-768(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Lin X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AC007017; AAD21470.1; -.  
 SQ SEQUENCE 36 AA; 4358 MW; DC966779BBD6B834 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29  
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Db 4 KKLQ 7

Search completed: January 14, 2004, 10:41:46  
Job time : 50.4206 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 5.61371 Seconds  
 (without alignments)  
 284.822 Million cell updates/sec

Title: US-09-843-221A-161  
 Perfect score: 34  
 Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28  
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%				
No.	Score	Query	Match	Length	ID	Description
1	5	14.7	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	11.8	29	1	DMD_RAT	P11530 rattus norv
3	4	11.8	39	1	PSBY_SYNY3	P73676 synechocyst
4	4	11.8	39	1	SR1C_SARPE	P08377 sarcophaga
5	3	8.8	28	1	CH60_MYCSM	P80673 mycobacteri
6	3	8.8	28	1	COXB_SOLTU	P80499 solanum tub
7	3	8.8	28	1	GUN_SCHCO	P81190 schizophyll
8	3	8.8	28	1	PA23_TRIST	P82894 trimeresuru
9	3	8.8	28	1	PA2C_PSEPO	P20260 pseudechis
10	3	8.8	28	1	VI03_VACCP	Q00334 vaccinia vi
11	3	8.8	28	1	VIP_ALLMI	P48142 alligator m
12	3	8.8	28	1	VIP_RANRI	P81016 rana ridibu
13	3	8.8	28	1	VIP_SHEEP	P04565 ovis aries
14	3	8.8	29	1	GALA_ALLMI	P47215 alligator m
15	3	8.8	29	1	GALA_AMICA	P47214 amia calva
16	3	8.8	29	1	GALA_CHICK	P30802 gallus gall
17	3	8.8	29	1	GALA_ONCMY	P47213 oncorhynch

18	3	8.8	29	1	GALA_RANRI	P47216	rana ridibu
19	3	8.8	29	1	GALA_SHEEP	P31234	ovis aries
20	3	8.8	29	1	GLUC_CHIBR	P31297	chinchilla
21	3	8.8	29	1	IPYR_DESVH	P19371	desulfovibr
22	3	8.8	29	1	NUO1_SOLTU	P80267	solanum tub
23	3	8.8	29	1	P2SM_LOXIN	P83046	loxosceles
24	3	8.8	29	1	PCG4_PACGO	P82417	pachycondyl
25	3	8.8	29	1	RS7_METTE	O93639	methanosarc
26	3	8.8	29	1	SODC_OLEEU	P80740	olea europa
27	3	8.8	29	1	TL16_SPIOL	P81834	spinacia ol
28	3	8.8	30	1	DMS3_PHYSA	P80279	phyllomedus
29	3	8.8	30	1	FTN_BACFR	P28733	bacteroides
30	3	8.8	30	1	GLUM_ANGAN	P41521	anguilla an
31	3	8.8	30	1	OTCC_AERPU	P11726	aeromonas p
32	3	8.8	30	1	PCG2_PACGO	P82415	pachycondyl
33	3	8.8	30	1	PCG3_PACGO	P82416	pachycondyl
34	3	8.8	30	1	PSAM_PORPU	P51395	porphyra pu
35	3	8.8	30	1	TX2_THRPR	P83476	thrixopelma
36	3	8.8	30	1	UP61_UPEIN	P82037	uperoleia i
37	3	8.8	30	1	UP62_UPEIN	P82038	uperoleia i
38	3	8.8	30	1	VAA2_EQUAR	Q04238	equisetum a
39	3	8.8	30	1	Y523_BORBU	O51473	borrelia bu
40	3	8.8	31	1	CEC1_PIG	P14661	sus scrofa
41	3	8.8	31	1	CXMA_CONMR	P56708	conus marmo
42	3	8.8	31	1	DEJP_DROME	P81160	drosophila
43	3	8.8	31	1	DIUX_DIPPU	P82372	diploptera
44	3	8.8	31	1	H13_WHEAT	P15872	triticum ae
45	3	8.8	31	1	LPL_BUCRP	Q53017	buchnera ap
46	3	8.8	31	1	MALK_PHOLU	P41124	photorhabdu
47	3	8.8	31	1	NAP4_HUMAN	P19877	homo sapien
48	3	8.8	31	1	PETL_LOTJA	Q9bbr4	lotus japon
49	3	8.8	31	1	PETL_MARPO	P12179	marchantia
50	3	8.8	31	1	PETL_MESVI	Q9mun4	mesostigma
51	3	8.8	31	1	PETL_NEPOL	Q9tky9	nephroselmi
52	3	8.8	31	1	PSAM_EUGGR	P31479	euglena gra
53	3	8.8	31	1	SARL_MOUSE	Q9cqd6	mus musculu
54	3	8.8	31	1	SARL_RABIT	P42532	oryctolagus
55	3	8.8	31	1	SCK5_ANDMA	P31719	androctonus
56	3	8.8	31	1	SCKL_LEIQH	P16341	leiurus qui
57	3	8.8	31	1	Y822_BORBU	O51762	borrelia bu
58	3	8.8	32	1	ADHR_DROYA	P28487	drosophila
59	3	8.8	32	1	CAL2_ONCKE	P01264	oncorhynchu
60	3	8.8	32	1	CAL3_ONCKI	P01265	oncorhynchu
61	3	8.8	32	1	CAL_ANGJA	P01262	anguilla ja
62	3	8.8	32	1	COA2_BPIF1	O80296	bacterioph
63	3	8.8	32	1	CY31_DESAC	P81078	desulfuromo
64	3	8.8	32	1	FF21_SALEN	P55224	salmonella
65	3	8.8	32	1	IAPP_PIG	Q29119	sus scrofa
66	3	8.8	32	1	ITR3_CUCPE	P10293	cucurbita p
67	3	8.8	32	1	ITR4_CUCMA	P07853	cucurbita m
68	3	8.8	32	1	LEC_DOLAX	P02875	dolichos ax
69	3	8.8	32	1	MIFH_TRITR	P81748	trichuris t
70	3	8.8	32	1	P1SM_LOXIN	P83045	loxosceles
71	3	8.8	32	1	PETM_GUITH	O78499	guillardia
72	3	8.8	32	1	PHSS_DESBN	P13064	desulfovibr
73	3	8.8	32	1	PSAM_MARPO	P31590	marchantia
74	3	8.8	32	1	PSBQ_PEA	P19589	pisum sativ



75	3	8.8	32	1	PSBT_ODOSI	P49516	odontella s
76	3	8.8	32	1	PSBZ_EUGST	Q8sl89	euglena ste
77	3	8.8	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
78	3	8.8	32	1	Y160_BPT4	P39247	bacterioph
79	3	8.8	32	1	YCPG_MASLA	P29735	mastigoclad
80	3	8.8	33	1	GGN1_RANRU	P80395	rana rugosa
81	3	8.8	33	1	GLU2_ORENI	P81027	oreochromis
82	3	8.8	33	1	RUGB_RANRU	P80955	rana rugosa
83	3	8.8	33	1	T1F_PARTE	Q27172	paramecium
84	3	8.8	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
85	3	8.8	33	1	YC12_EUGGR	P31559	euglena gra
86	3	8.8	34	1	DMS1_PHYSA	P24302	phyllomedus
87	3	8.8	34	1	DMS2_PHYSA	P80278	phyllomedus
88	3	8.8	34	1	GAST_CAPHI	P04564	capra hircu
89	3	8.8	34	1	GUN1_SCLSC	P21833	sclerotinia
90	3	8.8	34	1	TX1_SCOGR	P56855	scodra gris
91	3	8.8	35	1	CECA_AEDAL	P81417	aedes albop
92	3	8.8	35	1	COPA_CANFA	P40765	canis famil
93	3	8.8	35	1	CPI2_PIG	P80736	sus scrofa
94	3	8.8	35	1	GP58_BPSP1	O48412	bacterioph
95	3	8.8	35	1	HCYA_CHEDE	P83173	cherax dest
96	3	8.8	35	1	LEC1_CYTSE	P22970	cytisis ses
97	3	8.8	35	1	LEC3_ULEEU	P23032	ulex europe
98	3	8.8	35	1	NP30_STAAU	P21222	staphylococ
99	3	8.8	35	1	PBP_ORGPS	P34178	orgyia pseu
100	3	8.8	35	1	PETG_CYACA	Q9tlq9	cyanidium c
101	3	8.8	35	1	PSBM_SYNY3	P72701	synechocyst
102	3	8.8	35	1	RL15_SYNP7	P31160	synechococc
103	3	8.8	35	1	SCKK_TITSE	P56219	tityus serr
104	3	8.8	35	1	TX1_GRASP	P56852	grammostola
105	3	8.8	35	1	TX1_THRPR	P83480	thrixopelma
106	3	8.8	35	1	TX2_GRASP	P56853	grammostola
107	3	8.8	35	1	VORB_METTM	P80908	methanobact
108	3	8.8	35	1	Y210_HAEIN	P43964	haemophilus
109	3	8.8	35	1	YRKM_BACSU	P54440	bacillus su
110	3	8.8	36	1	ELH_THETS	P80594	theromyzon
111	3	8.8	36	1	NPF_ARTTR	P41334	artioposthi
112	3	8.8	36	1	OSTS_YEAST	Q99380	saccharomyc
113	3	8.8	36	1	PETM_SYNY3	P74810	synechocyst
114	3	8.8	36	1	R18A_BOVIN	P82919	bos taurus
115	3	8.8	36	1	RET4_CHICK	P30370	gallus gall
116	3	8.8	36	1	RL6_HALCU	P05968	halobacteri
117	3	8.8	36	1	Y260_BACHD	Q9kg53	bacillus ha
118	3	8.8	36	1	Y609_ARCFU	O29646	archaeoglob
119	3	8.8	37	1	DIU1_TENMO	P56618	tenebrio mo
120	3	8.8	37	1	IAPP_CRIGR	P19890	cricetulus
121	3	8.8	37	1	LCNM_LACLA	P83002	lactococcus
122	3	8.8	37	1	OGT1_RABIT	P81436	oryctolagus
123	3	8.8	37	1	PIP7_BOVIN	P21671	bos taurus
124	3	8.8	37	1	RL36_PASMU	P57942	pasteurella
125	3	8.8	37	1	SCKI_MESTA	P24663	mesobuthus
126	3	8.8	37	1	Y63_BPT3	P20328	bacterioph
127	3	8.8	38	1	CPRP_CANPG	P81033	cancer pagu
128	3	8.8	38	1	DNP_DENAN	P28374	dendroaspis
129	3	8.8	38	1	NLT1_VITSX	P80275	vitis sp. (
130	3	8.8	38	1	NLT2_VITSX	P33556	vitis sp. (
131	3	8.8	38	1	OBP2_HYSCR	P81648	hystrix cri

132	3	8.8	38	1	PYSA_METBA	P80521	methanosarc
133	3	8.8	38	1	RL36_ECOLI	P21194	escherichia
134	3	8.8	38	1	RL36_PSEAE	Q9hwf6	pseudomonas
135	3	8.8	38	1	RL36_THEMA	Q9xli6	thermotoga
136	3	8.8	38	1	RL36_YERPE	Q8zj91	yersinia pe
137	3	8.8	38	1	RR12_PINCO	P49168	pinus conto
138	3	8.8	38	1	YJ39_ARCFU	O28340	archaeoglob
139	3	8.8	39	1	CEC_GLOMR	P83403	glossina mo
140	3	8.8	39	1	COLI_BALPH	P01195	balaenopter
141	3	8.8	39	1	COLI_RABIT	P06297	oryctolagus
142	3	8.8	39	1	COLI_SQUAC	P01197	squalus aca
143	3	8.8	39	1	COLI_STRCA	P01196	struthio ca
144	3	8.8	39	1	EXE3_HELHO	P20394	heloderma h
145	3	8.8	39	1	FUC3_RAT	P80349	rattus norv
146	3	8.8	39	1	GVPC_SPICC	P81000	spirulina s
147	3	8.8	39	1	H2A_BUFBG	P55897	bufo bufo g
148	3	8.8	39	1	LCGA_LACLA	P36961	lactococcus
149	3	8.8	39	1	PA2_AGKBI	Q9psf9	agkistrodon
150	3	8.8	39	1	PSBX_PORPU	P51197	porphyra pu
151	3	8.8	40	1	ALB1_TRASC	P81188	trachemys s
152	3	8.8	40	1	HPT_RABIT	P19007	oryctolagus
153	3	8.8	40	1	HS9A_RABIT	P30946	oryctolagus
154	3	8.8	40	1	KAD_STACA	P35141	staphylococ
155	3	8.8	40	1	PHRK_BACSU	O31840	bacillus su
156	3	8.8	40	1	PRE_BACLI	P18189	bacillus li
157	3	8.8	40	1	RK33_PEA	P51416	pisum sativ
158	3	8.8	40	1	RRPO_LSV	P27328	lily sympto
159	3	8.8	40	1	SAUV_PHYSA	P01144	phyllomedus
160	3	8.8	40	1	SR1D_SARPE	P18312	sarcophaga
161	3	8.8	40	1	UC11_MAIZE	P80617	zea mays (m
162	3	8.8	40	1	VIT_MELGA	P56531	meleagris g
163	3	8.8	40	1	YDRB_STRPE	P32012	streptomyce
164	2	5.9	28	1	ACON_CANAL	P82611	candida alb
165	2	5.9	28	1	APC1_RABIT	P33047	oryctolagus
166	2	5.9	28	1	ARYC_NOCGL	P80008	nocardia gl
167	2	5.9	28	1	C1QC_RAT	P31722	rattus norv
168	2	5.9	28	1	ETX2_BACCE	P80568	bacillus ce
169	2	5.9	28	1	FIBA_CANFA	P02673	canis famil
170	2	5.9	28	1	FLA1_TREPH	P21988	treponema p
171	2	5.9	28	1	GDO_TRIMO	P02865	triticum mo
172	2	5.9	28	1	GRP_ALLMI	P31886	alligator m
173	2	5.9	28	1	GTS5_CHICK	P20137	gallus gall
174	2	5.9	28	1	GVPC_OSCAG	P80999	oscillator
175	2	5.9	28	1	HORC_HORSP	P02864	hordeum spo
176	2	5.9	28	1	ICPP_VIPLE	P82475	vipera lebe
177	2	5.9	28	1	IEL1_MOMCH	P10296	momordica c
178	2	5.9	28	1	IORB_METTM	P80911	methanobact
179	2	5.9	28	1	ITR2_MOMCH	P10295	momordica c
180	2	5.9	28	1	ITR3_LUFCY	P35628	luffa cylin
181	2	5.9	28	1	ITRA_MOMCH	P30709	momordica c
182	2	5.9	28	1	LECA_IRIHO	P36230	iris hollan
183	2	5.9	28	1	LPFS_ECOLI	P22183	escherichia
184	2	5.9	28	1	LPL_ECOLI	P09149	escherichia
185	2	5.9	28	1	LPL_SALTI	Q8z9h9	salmonella
186	2	5.9	28	1	LPL_SALTY	P03062	salmonella
187	2	5.9	28	1	LPW_SERMA	P03055	serratia ma
188	2	5.9	28	1	MAAI_RAT	P57113	rattus norv

189	2	5.9	28	1	MCDP_MEGPE	P04567	megabombus
190	2	5.9	28	1	NLT2_WHEAT	P39085	triticum ae
191	2	5.9	28	1	NXL1_BOUAN	P34074	boulengerin
192	2	5.9	28	1	OBP1_HYSCR	P81647	hystrix cri
193	2	5.9	28	1	OMPA_YERPS	P38399	yersinia ps
194	2	5.9	28	1	ORND_PLAOR	P25513	placobdella
195	2	5.9	28	1	OST1_CHICK	P80896	gallus gall
196	2	5.9	28	1	PA22_MICNI	P21791	micrurus ni
197	2	5.9	28	1	PA23_MICNI	P21792	micrurus ni
198	2	5.9	28	1	PETL_CYAPA	P48102	cyanophora
199	2	5.9	28	1	PHR_METTM	P58818	methanobact
200	2	5.9	28	1	PHYB_ASPFI	P81440	aspergillus
201	2	5.9	28	1	PP71_HCMVT	P24429	human cytom
202	2	5.9	28	1	PPOX_BOVIN	P56602	bos taurus
203	2	5.9	28	1	RL5_HALCU	P05972	halobacteri
204	2	5.9	28	1	RS19_PHYS1	O66093	phytoplasma
205	2	5.9	28	1	SCX2_BUTSI	P15230	buthus sind
206	2	5.9	28	1	SLP1_LEIQH	P80669	leiurus qui
207	2	5.9	28	1	SMS2_ORENI	P81029	oreochromis
208	2	5.9	28	1	TXO2_AGEAP	P15971	agelenopsis
209	2	5.9	28	1	VG9_SPV4	P11341	spiroplasma
210	2	5.9	28	1	VIP_DIDMA	P39089	didelphis m
211	2	5.9	28	1	VIP_SCYCA	P09685	scyliorhinu
212	2	5.9	28	1	Y073_ARCFU	O30163	archaeoglob
213	2	5.9	28	1	Y16P_BPT4	P39248	bacterioph
214	2	5.9	28	1	YA79_ARCFU	O29184	archaeoglob
215	2	5.9	29	1	12AH_CLOS4	P21215	clostridium
216	2	5.9	29	1	AL21_HORSE	P81216	equus cabal
217	2	5.9	29	1	AMEL_RABIT	P12761	oryctolagus
218	2	5.9	29	1	ATP9_PICPJ	Q06838	pichia pijp
219	2	5.9	29	1	ATPA_BRYMA	P26965	bryopsis ma
220	2	5.9	29	1	BR2D_RANES	P40840	rana escule
221	2	5.9	29	1	BREE_RANES	P40841	rana escule
222	2	5.9	29	1	CERB_CERCA	P36191	ceratitidis c
223	2	5.9	29	1	COA1_BPI22	P15413	bacterioph
224	2	5.9	29	1	COXJ_CANFA	Q9tr29	canis famil
225	2	5.9	29	1	COXK_SHEEP	Q9tr28	ovis aries
226	2	5.9	29	1	CU36_LOCFI	P11737	locusta mig
227	2	5.9	29	1	CXD6_CONGL	Q9twm7	conus glori
228	2	5.9	29	1	CXOC_CONMA	P37300	conus magus
229	2	5.9	29	1	CXOD_CONMA	Q26350	conus magus
230	2	5.9	29	1	CXST_CONGE	P58844	conus geogr
231	2	5.9	29	1	DMS5_PHYSA	P80281	phyllomedus
232	2	5.9	29	1	GLUC_ANAPL	P01276	anas platyr
233	2	5.9	29	1	GLUC_CALMI	P13189	callorhynch
234	2	5.9	29	1	GLUC_DIDMA	P18108	didelphis m
235	2	5.9	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
236	2	5.9	29	1	GLUC_PLAFE	P23062	platichthys
237	2	5.9	29	1	GLUC_RABIT	P25449	oryctolagus
238	2	5.9	29	1	GLUC_TORMA	P09567	torpedo mar
239	2	5.9	29	1	H2B2_ECHES	P13282	echinus esc
240	2	5.9	29	1	HOXY_RHOOP	P22660	rhodococcus
241	2	5.9	29	1	HRJ_BOTJA	P20416	bothrops ja
242	2	5.9	29	1	HS98_NEUCR	P31540	neurospora
243	2	5.9	29	1	ITH3_BOVIN	P56652	bos taurus
244	2	5.9	29	1	ITR1_CUCMA	P01074	cucurbita m
245	2	5.9	29	1	ITR1_LUFCY	P25849	luffa cylin

246	2	5.9	29	1	ITR1_MOMRE	P17680	momordica r
247	2	5.9	29	1	ITR2_BRYDI	P11968	bryonia dio
248	2	5.9	29	1	ITR3_CYCPE	P83394	cyclanthera
249	2	5.9	29	1	ITR4_CYCPE	P83395	cyclanthera
250	2	5.9	29	1	ITR5_CYCPE	P83396	cyclanthera
251	2	5.9	29	1	KDPF_ECOLI	P36937	escherichia
252	2	5.9	29	1	MDH_BURPS	P80536	burkholderi
253	2	5.9	29	1	MULR_ECHML	P81798	echis multi
254	2	5.9	29	1	PETN_ANASP	Q913p6	anabaena sp
255	2	5.9	29	1	PETN_ARATH	P12178	arabidopsis
256	2	5.9	29	1	PETN_CHAGL	Q8ma13	chaetosphae
257	2	5.9	29	1	PETN_CYAPA	P48258	cyanophora
258	2	5.9	29	1	PETN_GUITH	O78498	guillardia
259	2	5.9	29	1	PETN_MAIZE	Q33302	zea mays (m
260	2	5.9	29	1	PETN_MARPO	P12177	marchantia
261	2	5.9	29	1	PETN_MESVI	Q9mus4	mesostigma
262	2	5.9	29	1	PETN_ODOSI	P49527	odontella s
263	2	5.9	29	1	PETN_PINTH	P41611	pinus thunb
264	2	5.9	29	1	PETN_PORPU	P51276	porphyra pu
265	2	5.9	29	1	PETN_PSINU	Q8wi23	psilotum nu
266	2	5.9	29	1	PETN_SKECO	O96807	skeletonema
267	2	5.9	29	1	PETN_SYNEL	Q8dkn2	synechococc
268	2	5.9	29	1	PETN_SYNY3	P72717	synechocyst
269	2	5.9	29	1	PK4_DICDI	P34103	dictyosteli
270	2	5.9	29	1	PRO1_DACGL	P18689	dactylis gl
271	2	5.9	29	1	PSAF_SYNP6	P31083	synechococc
272	2	5.9	29	1	PSAK_SPIOL	P14627	spinacia ol
273	2	5.9	29	1	PSAM_GUITH	O78448	guillardia
274	2	5.9	29	1	PSAX_SYNVU	P23320	synechococc
275	2	5.9	29	1	PSBI_SYNVU	P12240	synechococc
276	2	5.9	29	1	RL15_HALCU	P05971	halobacteri
277	2	5.9	29	1	RL15_STRLI	P49975	streptomyce
278	2	5.9	29	1	RP54_CLOKL	P38944	clostridium
279	2	5.9	29	1	SCX1_ANDMA	P56215	androctonus
280	2	5.9	29	1	SDHB_CLOPR	P80213	clostridium
281	2	5.9	29	1	SLP2_LEIQH	P80670	leiurus qui
282	2	5.9	29	1	SLP3_LEIQH	P80671	leiurus qui
283	2	5.9	29	1	TAT_HV1Z3	P12510	human immun
284	2	5.9	29	1	TLP_ACTDE	P81370	actinidia d
285	2	5.9	29	1	VARF_VIOAR	P58451	viola arven
286	2	5.9	29	1	Y15_BPT7	P03792	bacterioph
287	2	5.9	29	1	Y51_BPT3	P20326	bacterioph
288	2	5.9	29	1	YCX4_ODOSI	P49830	odontella s
289	2	5.9	29	1	YCX4_ODOSI	P49838	odontella s
290	2	5.9	30	1	2ENR_CLOTY	P11887	clostridium
291	2	5.9	30	1	A1AT_CHIVI	P38026	chinchilla
292	2	5.9	30	1	AATC_RABIT	P12343	oryctolagus
293	2	5.9	30	1	AATM_RABIT	P12345	oryctolagus
294	2	5.9	30	1	ACB1_DIGLA	P81624	digitalis l
295	2	5.9	30	1	AMPT_BACST	P00728	bacillus st
296	2	5.9	30	1	ANF_RANRI	P09196	rana ridibu
297	2	5.9	30	1	CALM_LYTPI	P05935	lytechinus
298	2	5.9	30	1	CBAL_BACST	P13722	bacillus st
299	2	5.9	30	1	CH60_CLOPA	P81339	clostridium
300	2	5.9	30	1	CIRA_CHAPA	P56871	chassalia p
301	2	5.9	30	1	CLPA_PINPS	P81671	pinus pinas
302	2	5.9	30	1	COAE_CORAM	P58101	corynebacte

303	2	5.9	30	1	COXC_SOLTU	P80500	solanum tub
304	2	5.9	30	1	CRG2_SCOWA	P19865	scoliodon w
305	2	5.9	30	1	CX2A_CONBE	P58625	conus betul
306	2	5.9	30	1	CX7A_CONTU	P58923	conus tulip
307	2	5.9	30	1	CXEX_CONCN	P58928	conus conso
308	2	5.9	30	1	CXK4_CONST	P58921	conus stria
309	2	5.9	30	1	CXOB_CONPE	P56713	conus penna
310	2	5.9	30	1	CXVB_CONER	P58783	conus ermin
311	2	5.9	30	1	CY35_DESAC	P81079	desulfuromo
312	2	5.9	30	1	CY01_VIOOD	P82230	viola odora
313	2	5.9	30	1	CY08_VIOOD	P58440	viola odora
314	2	5.9	30	1	DEF2_MACMU	P82317	macaca mula
315	2	5.9	30	1	DIDH_COMTE	P80702	comamonas t
316	2	5.9	30	1	DIU2_HYLLI	P82015	hyles linea
317	2	5.9	30	1	DIU2_MANSE	P24858	manduca sex
318	2	5.9	30	1	END2_ONCKE	P01205	oncorhynchu
319	2	5.9	30	1	FIBR_PANIN	P22775	panulirus i
320	2	5.9	30	1	HCY2_HOMAM	P82297	homarus ame
321	2	5.9	30	1	HETA_RADMA	P58691	radianthus
322	2	5.9	30	1	HYPH_HYBPA	P58445	hybanthus p
323	2	5.9	30	1	IHFB_RHILE	P80606	rhizobium l
324	2	5.9	30	1	ITI1_LAGLE	P26771	lagenaria l
325	2	5.9	30	1	ITR1_CITLA	P11969	citrullus l
326	2	5.9	30	1	ITR1_MOMCH	P10294	momordica c
327	2	5.9	30	1	ITR2_ECBEL	P12071	ecballium e
328	2	5.9	30	1	ITR2_LUFCY	P25850	luffa cylin
329	2	5.9	30	1	ITR3_CUCMC	P32041	cucumis mel
330	2	5.9	30	1	ITR3_MOMCO	P82410	momordica c
331	2	5.9	30	1	ITR4_CUCSA	P10292	cucumis sat
332	2	5.9	30	1	ITR6_CYCPE	P83397	cyclanthera
333	2	5.9	30	1	ITR7_CYCPE	P83398	cyclanthera
334	2	5.9	30	1	KAB5_OLDAF	P58456	oldenlandia
335	2	5.9	30	1	LAS1_PIG	P80171	sus scrofa
336	2	5.9	30	1	LEAH_PHAVU	P81870	phaseolus v
337	2	5.9	30	1	MDH_HELGE	P80037	heliobacter
338	2	5.9	30	1	MMAL_DERMI	P16312	dermatophag
339	2	5.9	30	1	NU5M_PISOC	P24999	pisaster oc
340	2	5.9	30	1	NUO2_SOLTU	P80268	solanum tub
341	2	5.9	30	1	P2CO_ARTSP	P37365	arthrobacte
342	2	5.9	30	1	PCCA_MYXXA	P81185	myxococcus
343	2	5.9	30	1	PCG1_PACGO	P82414	pachycondyl
344	2	5.9	30	1	PCG5_PACGO	P82418	pachycondyl
345	2	5.9	30	1	PETN_NEPOL	Q9t101	nephroselmi
346	2	5.9	30	1	PLF4_RABIT	P83470	oryctolagus
347	2	5.9	30	1	PLMS_SQUAC	P82542	squalus aca
348	2	5.9	30	1	PMGY_CANAL	P82612	candida alb
349	2	5.9	30	1	PRT1_CLUPA	P02335	clupea pall
350	2	5.9	30	1	PRT2_ONCMY	P02331	oncorhynchu
351	2	5.9	30	1	PRT3_ONCMY	P02332	oncorhynchu
352	2	5.9	30	1	PRT4_ONCMY	P02333	oncorhynchu
353	2	5.9	30	1	PRTB_ONCMY	P12819	oncorhynchu
354	2	5.9	30	1	PSAM_CYACA	Q9t1x5	cyanidium c
355	2	5.9	30	1	PSAM_MESVI	Q9mus2	mesostigma
356	2	5.9	30	1	PSAM_ODOSI	P49487	odontella s
357	2	5.9	30	1	PSAM_PINTH	P41601	pinus thunb
358	2	5.9	30	1	PYSD_METBA	P80524	methanosarc
359	2	5.9	30	1	RIPS_MOMCO	P20655	momordica c

360	2	5.9	30	1	RKGG_LEPKE	P21587	lepidochely
361	2	5.9	30	1	RNP_ODOVI	P19640	odocoileus
362	2	5.9	30	1	SCK2_TITSE	P08816	tityus serr
363	2	5.9	30	1	SCX2_CENLI	P18927	centruroide
364	2	5.9	30	1	SILU_RHIPU	P02885	rhizomucor
365	2	5.9	30	1	TAT_HV1ZH	P12512	human immun
366	2	5.9	30	1	TL1X_SPIOL	P82537	spinacia ol
367	2	5.9	30	1	TL29_SPIOL	P81833	spinacia ol
368	2	5.9	30	1	TX2_HETVE	P58426	heteropoda
369	2	5.9	30	1	UC35_MAIZE	P80641	zea mays (m
370	2	5.9	30	1	UDDP_SULAC	P80143	sulfolobus
371	2	5.9	30	1	URE1_ECOLI	Q03284	escherichia
372	2	5.9	30	1	VAA1_EQUAR	Q04236	equisetum a
373	2	5.9	30	1	VAA1_PSINU	Q04237	psilotum nu
374	2	5.9	30	1	VAA2_PSINU	Q04239	psilotum nu
375	2	5.9	30	1	VATN_BOVIN	P81134	bos taurus
376	2	5.9	30	1	VG03_BPPF1	P25137	bacterioph
377	2	5.9	30	1	VPU_HV1SC	P05948	human immun
378	2	5.9	30	1	VTTA_BPT3	P20837	bacterioph
379	2	5.9	30	1	Y161_TREPA	O83196	treponema p
380	2	5.9	30	1	Y357_BORBU	O51332	borrelia bu
381	2	5.9	30	1	Y425_BORBU	O51386	borrelia bu
382	2	5.9	30	1	Y573_TREPA	O83583	treponema p
383	2	5.9	30	1	Y932_TREPA	O83902	treponema p
384	2	5.9	30	1	YCCB_ECOLI	P24244	escherichia
385	2	5.9	31	1	A98A_DROME	O46201	drosophila
386	2	5.9	31	1	BCAM_PIG	O19098	sus scrofa
387	2	5.9	31	1	CIRB_CHAPA	P56879	chassalia p
388	2	5.9	31	1	COG5_BOVIN	P83437	bos taurus
389	2	5.9	31	1	COX4_NEUCR	P06809	neurospora
390	2	5.9	31	1	CTRP_PENMO	P35002	penaeus mon
391	2	5.9	31	1	CU54_LOCFI	P11738	locusta mig
392	2	5.9	31	1	CXD6_CONNI	P56710	conus nigro
393	2	5.9	31	1	CXG6_CONTE	P58922	conus texti
394	2	5.9	31	1	CYLA_PSYLO	P56872	psychotria
395	2	5.9	31	1	DEF2_MESAU	P81466	mesocricetu
396	2	5.9	31	1	EFTU_STRLU	P52390	streptomyce
397	2	5.9	31	1	ENDB_CAMDR	P01203	camelus dro
398	2	5.9	31	1	ER29_BOVIN	P81623	bos taurus
399	2	5.9	31	1	ETFD_PARDE	P55932	paracoccus
400	2	5.9	31	1	FIBB_CANFA	P02677	canis famil
401	2	5.9	31	1	GP37_BPSP1	O48393	bacterioph
402	2	5.9	31	1	GT_SERMA	P22416	serratia ma
403	2	5.9	31	1	HBA_MACEU	P81043	macropus eu
404	2	5.9	31	1	HCY1_HOMAM	P82296	homarus ame
405	2	5.9	31	1	HCY2_MAISQ	P82303	maia squina
406	2	5.9	31	1	HEM2_PHAGO	P27687	phascolopsi
407	2	5.9	31	1	LC70_LACPA	P80959	lactobacill
408	2	5.9	31	1	LCCB_LEUME	P81052	leuconostoc
409	2	5.9	31	1	LPRM_ECOLI	P10739	escherichia
410	2	5.9	31	1	MDH_STRAR	P19982	streptomyce
411	2	5.9	31	1	PETL_ANASP	Q8yvq2	anabaena sp
412	2	5.9	31	1	PETL_ARATH	P56776	arabidopsis
413	2	5.9	31	1	PETL_BETVU	P46612	beta vulgar
414	2	5.9	31	1	PETL_CHLVU	P56306	chlorella v
415	2	5.9	31	1	PETL_GUITH	O78468	guillardia
416	2	5.9	31	1	PETL_MAIZE	P19445	zea mays (m

417	2	5.9	31	1	PETL_ODOSI	P49524	odontella s
418	2	5.9	31	1	PETL_OENHO	Q9mtk4	oenothera h
419	2	5.9	31	1	PETL_ORYSA	P12180	oryza sativ
420	2	5.9	31	1	PETL_PORPU	P51221	porphyra pu
421	2	5.9	31	1	PETL_PSINU	Q8wi03	psilotum nu
422	2	5.9	31	1	PETL_SPIOL	Q9m310	spinacia ol
423	2	5.9	31	1	PETL_WHEAT	P58247	triticum ae
424	2	5.9	31	1	PETM_CYACA	Q9t1r5	cyanidium c
425	2	5.9	31	1	PETN_CYACA	Q9t1r6	cyanidium c
426	2	5.9	31	1	PRT2_CLUPA	P02336	clupea pall
427	2	5.9	31	1	PSAK_ANAVA	P23317	anabaena va
428	2	5.9	31	1	PSAM_CHLVU	P56314	chlorella v
429	2	5.9	31	1	PSAM_CYAPA	P48185	cyanophora
430	2	5.9	31	1	PSBK_SYNVU	P19054	synechococc
431	2	5.9	31	1	PSBM_MESVI	Q9muq7	mesostigma
432	2	5.9	31	1	PSBT_CHLRE	P37256	chlamydomon
433	2	5.9	31	1	PSBT_CHLVU	P56327	chlorella v
434	2	5.9	31	1	PSBT_CYAPA	P48109	cyanophora
435	2	5.9	31	1	PSBT_EUGGR	P20176	euglena gra
436	2	5.9	31	1	PSBT_MESVI	Q9muv6	mesostigma
437	2	5.9	31	1	PSBT_PORPU	P51323	porphyra pu
438	2	5.9	31	1	PYSG_METBA	P80523	methanosarc
439	2	5.9	31	1	RECX_METCL	P37865	methylomona
440	2	5.9	31	1	RL21_STRTR	P48956	streptococc
441	2	5.9	31	1	SARL_HUMAN	O00631	homo sapien
442	2	5.9	31	1	SC37_MESMA	P83407	mesobuthus
443	2	5.9	31	1	SODC_STRHE	P81163	striga herm
444	2	5.9	31	1	TX3_HETVE	P58427	heteropoda
445	2	5.9	31	1	TXA3_PARAC	P09949	parascicyoni
446	2	5.9	31	1	Y191_BORBU	O51209	borrelia bu
447	2	5.9	31	1	Y3KD_BPCHP	P19187	bacterioph
448	2	5.9	31	1	Y603_ARCFU	O29652	archaeoglob
449	2	5.9	32	1	A2M_PACLE	P20738	pacifastacu
450	2	5.9	32	1	APL3_DIAGR	P81471	diatraea gr
451	2	5.9	32	1	ATP0_PIG	P80021	sus scrofa
452	2	5.9	32	1	ATP7_SPIOL	P80088	spinacia ol
453	2	5.9	32	1	ATPO_SPIOL	P80087	spinacia ol
454	2	5.9	32	1	B4G1_RAT	P80225	r beta-1,4-
455	2	5.9	32	1	CAAP_MICEC	P21162	micromonosp
456	2	5.9	32	1	CAL0_BOVIN	P01260	bos taurus
457	2	5.9	32	1	CAL0_PIG	P01259	sus scrofa
458	2	5.9	32	1	CAR1_ECHCA	Q9prp9	echis carin
459	2	5.9	32	1	CEC_OIKKI	P83420	oiketicus k
460	2	5.9	32	1	COA1_BPIF1	O80295	bacterioph
461	2	5.9	32	1	COA1_BPIKE	P03676	bacterioph
462	2	5.9	32	1	COA2_BPFD	P03677	bacterioph
463	2	5.9	32	1	CRP_PLEPL	P12245	pleuronecte
464	2	5.9	32	1	CXG7_CONPE	P56711	conus penna
465	2	5.9	32	1	CYBL_RHOGR	P32953	rhodotorula
466	2	5.9	32	1	CYSB_FASHE	P80529	fasciola he
467	2	5.9	32	1	DBH_SYNY1	P02343	synechocyst
468	2	5.9	32	1	ER29_CHICK	P81628	gallus gall
469	2	5.9	32	1	ER29_TRIVU	P81629	trichosurus
470	2	5.9	32	1	ERH_PIG	P80230	sus scrofa
471	2	5.9	32	1	FER_PORCR	P18821	porphyridiu
472	2	5.9	32	1	FLA1_METHU	P17603	methanospir
473	2	5.9	32	1	FRIH_ANAPL	P80145	anas platyr

474	2	5.9	32	1	GHR4_RAT	P33581	rattus norv
475	2	5.9	32	1	GLB4_LAMSP	P20413	lamellibrac
476	2	5.9	32	1	GT82_DICLA	P82608	dicentrarch
477	2	5.9	32	1	H2AZ_ONCMY	P22647	oncorhynchu
478	2	5.9	32	1	HCYC_CHEDE	P83172	cherax dest
479	2	5.9	32	1	IAPP_BOVIN	Q28207	bos taurus
480	2	5.9	32	1	IAPP_SAGOE	Q28934	saguinus oe
481	2	5.9	32	1	IAPP_SHEEP	Q28605	ovis aries
482	2	5.9	32	1	ILVB_ENTAE	Q09129	enterobacte
483	2	5.9	32	1	ITR2_CUCSA	P10291	cucumis sat
484	2	5.9	32	1	LPID_ECOLI	P03060	escherichia
485	2	5.9	32	1	LPID_EDWTA	P08140	edwardsiell
486	2	5.9	32	1	LPIV_ECOLI	P03061	escherichia
487	2	5.9	32	1	MDH_NITAL	P10887	nitzschia a
488	2	5.9	32	1	NEUB_PIG	P01297	sus scrofa
489	2	5.9	32	1	OVOS_ANAPL	P20739	anas platyr
490	2	5.9	32	1	PA22_AGKHP	P18997	agkistrodon
491	2	5.9	32	1	PA2_RHONO	P43318	rhopilema n
492	2	5.9	32	1	PETL_CHLRE	P50369	chlamydomon
493	2	5.9	32	1	PETM_PORPU	P51275	porphyra pu
494	2	5.9	32	1	PHNS_DESMU	P13062	desulfovibr
495	2	5.9	32	1	PRI3_ONCMY	P02330	oncorhynchu
496	2	5.9	32	1	PRT1_ONCKE	P02327	oncorhynchu
497	2	5.9	32	1	PRT4_SCYCA	P30259	scyliorhinu
498	2	5.9	32	1	PRT5_ONCMY	P02334	oncorhynchu
499	2	5.9	32	1	PRT6_ONCMY	P08145	oncorhynchu
500	2	5.9	32	1	PRT7_ONCMY	P08146	oncorhynchu
501	2	5.9	32	1	PRT8_ONCMY	P12817	oncorhynchu
502	2	5.9	32	1	PRT9_ONCMY	P08147	oncorhynchu
503	2	5.9	32	1	PRTA_ONCMY	P12818	oncorhynchu
504	2	5.9	32	1	PRTE_HALME	P28308	halobacteri
505	2	5.9	32	1	PRT_ORYLA	Q91185	oryzias lat
506	2	5.9	32	1	PSBT_CYACA	O19927	cyanidium c
507	2	5.9	32	1	PSBT_GUIITH	O78512	guillardia
508	2	5.9	32	1	PSBZ_EUGAN	Q8s195	euglena ana
509	2	5.9	32	1	PSBZ_EUGGA	Q8s193	euglena gra
510	2	5.9	32	1	PSBZ_EUGMY	Q8s191	euglena myx
511	2	5.9	32	1	RIP2_PHYDI	P34967	phytolacca
512	2	5.9	32	1	RK1_RABIT	P81655	oryctolagus
513	2	5.9	32	1	RS19_YEREN	Q56847	yersinia en
514	2	5.9	32	1	SCK2_CENNO	P58504	centruroides
515	2	5.9	32	1	TAT_SIVM2	P05912	simian immu
516	2	5.9	32	1	TRYP_PENMO	P35050	penaeus mon
517	2	5.9	32	1	TX29_PHONI	P29426	phoneutria
518	2	5.9	32	1	TXP7_APTSC	P49271	aptostichus
519	2	5.9	32	1	UC09_MAIZE	P80615	zea mays (m
520	2	5.9	32	1	Y169_TREPA	O83199	treponema p
521	2	5.9	32	1	Y433_BORBU	O51394	borrelia bu
522	2	5.9	32	1	YH17_HAEIN	P44295	haemophilus
523	2	5.9	32	1	YSCA_YEREN	Q01242	yersinia en
524	2	5.9	32	1	YTK3_ILTVT	P23985	infectious
525	2	5.9	33	1	ACT_DICVI	Q24733	dictyocaulu
526	2	5.9	33	1	ALOX_PICPA	P04842	pichia past
527	2	5.9	33	1	ANP3_MYOSC	P04367	myoxocephal
528	2	5.9	33	1	ANP5_MYOAE	P20421	myoxocephal
529	2	5.9	33	1	ATP7_SOLTU	P80496	solanum tub
530	2	5.9	33	1	BR2A_RANES	P40837	rana escule



531	2	5.9	33	1	BR2B_RANES	P40838	rana escule
532	2	5.9	33	1	BR2E_RANES	P32413	rana escule
533	2	5.9	33	1	BR2_RANBP	P32424	rana brevip
534	2	5.9	33	1	CECB_HELVI	P83414	heliiothis v
535	2	5.9	33	1	CECC_HELVI	P83415	heliiothis v
536	2	5.9	33	1	COA1_BPFD	P03675	bacterioph
537	2	5.9	33	1	COA2_BPI22	P15414	bacterioph
538	2	5.9	33	1	COA2_BPIKE	P03678	bacterioph
539	2	5.9	33	1	COXL_ONCMY	P80330	oncorhynch
540	2	5.9	33	1	CU89_HUMAN	P59042	homo sapien
541	2	5.9	33	1	CXBW_CONRA	P58804	conus radia
542	2	5.9	33	1	CXO_CONVE	P83301	conus ventr
543	2	5.9	33	1	DBB2_DOLAU	P83376	dolabella a
544	2	5.9	33	1	DEF1_MESAU	P81465	mesocricetu
545	2	5.9	33	1	DEF3_MESAU	P81467	mesocricetu
546	2	5.9	33	1	DEF4_MESAU	P81468	mesocricetu
547	2	5.9	33	1	DHE3_PIG	P42174	sus scrofa
548	2	5.9	33	1	FER_PORAE	P18820	porphyridiu
549	2	5.9	33	1	GAST_CAVPO	P06885	cavia porce
550	2	5.9	33	1	GAST_CHIBR	P10034	chinchilla
551	2	5.9	33	1	GAST_DIDMA	P33713	didelphis m
552	2	5.9	33	1	GGN2_RANRU	P80396	rana rugosa
553	2	5.9	33	1	GGN3_RANRU	P80397	rana rugosa
554	2	5.9	33	1	HF40_MAIZE	P82865	zea mays (m
555	2	5.9	33	1	HOXU_RHOOP	P22659	rhodococcus
556	2	5.9	33	1	LPPY_SALTY	P08522	salmonella
557	2	5.9	33	1	LPRH_ECOLI	P37324	escherichia
558	2	5.9	33	1	LYC2_HORSE	P81710	equus cabal
559	2	5.9	33	1	MBP1_MAIZE	P28794	zea mays (m
560	2	5.9	33	1	MHAA_STRCH	P80435	streptomyce
561	2	5.9	33	1	MYMY_MYTED	P81614	mytilus edu
562	2	5.9	33	1	OTCC_PSEPU	P11727	pseudomonas
563	2	5.9	33	1	PEN3_ADECU	P35987	canine aden
564	2	5.9	33	1	PETM_CYAPA	P48366	cyanophora
565	2	5.9	33	1	PETM_SYNEL	Q8dj15	synechococc
566	2	5.9	33	1	PK1_DICDI	P34101	dictyosteli
567	2	5.9	33	1	PK5_DICDI	P34104	dictyosteli
568	2	5.9	33	1	PRI1_ONCMY	P02326	oncorhynch
569	2	5.9	33	1	PRI2_ONCMY	P02328	oncorhynch
570	2	5.9	33	1	PRTB_MUGCE	P08130	mugil cepha
571	2	5.9	33	1	PRTL_ECOLI	P02338	escherichia
572	2	5.9	33	1	PSAI_SPIOL	P17228	spinacia ol
573	2	5.9	33	1	PSAK_CUCSA	P42051	cucumis sat
574	2	5.9	33	1	PSBT_ARATH	P37259	arabidopsis
575	2	5.9	33	1	PSBT_MAIZE	P37257	zea mays (m
576	2	5.9	33	1	RL21_XENLA	P49628	xenopus lae
577	2	5.9	33	1	RL26_XENLA	P49629	xenopus lae
578	2	5.9	33	1	RL28_XENLA	P46780	xenopus lae
579	2	5.9	33	1	RL4_HALCU	P05967	halobacteri
580	2	5.9	33	1	RPOC_HETCA	P36441	heterosigma
581	2	5.9	33	1	RRPO_BPBZ1	P09674	bacterioph
582	2	5.9	33	1	RS4_XENLA	P49401	xenopus lae
583	2	5.9	33	1	RT25_BOVIN	P82669	bos taurus
584	2	5.9	33	1	RUGA_RANRU	P80954	rana rugosa
585	2	5.9	33	1	SCX9_BUTOC	P04099	buthus occi
586	2	5.9	33	1	THIO_CLOST	P81109	clostridium
587	2	5.9	33	1	TX1_HETVE	P58425	heteropoda

588	2	5.9	33	1	TXH1_SELHU	P56676	selenocosmi
589	2	5.9	33	1	TXN3_SELHA	P83464	selenocosmi
590	2	5.9	33	1	VT1B_RAT	P58200	rattus norv
591	2	5.9	33	1	Y474_BORBU	051430	borrelia bu
592	2	5.9	33	1	Y656_TREPA	083662	treponema p
593	2	5.9	33	1	Y849_BORBU	051789	borrelia bu
594	2	5.9	33	1	YC12_CHLRE	P50370	chlamydomon
595	2	5.9	33	1	YC12_MARPO	P31560	marchantia
596	2	5.9	33	1	YC12_MESVI	Q9mus3	mesostigma
597	2	5.9	33	1	YC12_NEPOL	Q9tky6	nephroselmi
598	2	5.9	33	1	YC12_PINTH	P41600	pinus thunb
599	2	5.9	33	1	YL74_ARCFU	028108	archaeoglob
600	2	5.9	33	1	YLCH_BP82	Q37869	bacterioph
601	2	5.9	33	1	YLCH_ECOLI	Q47268	escherichia
602	2	5.9	34	1	AMP2_CHICK	P80390	gallus gall
603	2	5.9	34	1	ASPG_PIG	P30918	sus scrofa
604	2	5.9	34	1	BR2C_RANES	P40839	rana escule
605	2	5.9	34	1	COL_CHICK	P11148	gallus gall
606	2	5.9	34	1	COXA_THETH	P82543	thermus the
607	2	5.9	34	1	COXG_THUOB	P80976	thunnus obe
608	2	5.9	34	1	CXGS_CONGE	P15472	conus geogr
609	2	5.9	34	1	DEF2_RABIT	P07468	oryctolagus
610	2	5.9	34	1	DEF7_RABIT	P80223	oryctolagus
611	2	5.9	34	1	ECAB_ECTTU	P49344	ectatomma t
612	2	5.9	34	1	EF2_RABIT	P55823	oryctolagus
613	2	5.9	34	1	EGGR_APLCA	P01363	aplysia cal
614	2	5.9	34	1	H1S_STRPU	P19376	strongyloce
615	2	5.9	34	1	HS7S_CUCMA	P31082	cucurbita m
616	2	5.9	34	1	ITR1_MOMCO	P82408	momordica c
617	2	5.9	34	1	ITR2_MOMCO	P82409	momordica c
618	2	5.9	34	1	LPTN_PROVU	P28779	proteus vul
619	2	5.9	34	1	M44E_HUMAN	Q96pgl	homo sapien
620	2	5.9	34	1	MYTB_MYTED	P81613	mytilus edu
621	2	5.9	34	1	PETM_ANASP	Q9f4w2	anabaena sp
622	2	5.9	34	1	PRT1_SAROR	P25327	sarda orien
623	2	5.9	34	1	PRT1_SCOSC	P83264	scomber sco
624	2	5.9	34	1	PRT1_THUTH	P02321	thunnus thy
625	2	5.9	34	1	PRT2_SCOSC	P83265	scomber sco
626	2	5.9	34	1	PRT2_THUTH	P02322	thunnus thy
627	2	5.9	34	1	PRT_DICLA	Q9ps27	dicentrarch
628	2	5.9	34	1	PRT_PERFV	P29629	perca flave
629	2	5.9	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
630	2	5.9	34	1	PSAI_OENHO	Q9mtl2	oenothera h
631	2	5.9	34	1	PSAI_SOYBN	P49159	glycine max
632	2	5.9	34	1	PSBM_ARATH	P12169	arabidopsis
633	2	5.9	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
634	2	5.9	34	1	PSBM_CHLRE	P92277	chlamydomon
635	2	5.9	34	1	PSBM_MAIZE	P48189	zea mays (m
636	2	5.9	34	1	PSBM_MARPO	P12168	marchantia
637	2	5.9	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
638	2	5.9	34	1	PSBM_OENHO	Q9mtm8	oenothera h
639	2	5.9	34	1	PSBM_PEA	P34833	pisum sativ
640	2	5.9	34	1	PSBM_PSINU	Q8wi22	psilotum nu
641	2	5.9	34	1	PSBM_WHEAT	Q9xps6	triticum ae
642	2	5.9	34	1	PSBT_TOBAC	P12184	nicotiana t
643	2	5.9	34	1	PSPC_BOVIN	P15783	bos taurus
644	2	5.9	34	1	PSPC_CANFA	P22397	canis famil

645	2	5.9	34	1	PYSB_METBA	P80522	methanosarc
646	2	5.9	34	1	RNL1_PIG	P15466	sus scrofa
647	2	5.9	34	1	RR2_OCHNE	Q40606	ochrosphaer
648	2	5.9	34	1	SCXM_SCOMA	P80719	scorpio mau
649	2	5.9	34	1	SMS_MYXGL	P19209	myxine glut
650	2	5.9	34	1	THEM_MALSU	P13858	malbranchea
651	2	5.9	34	1	TX33_PHONI	P81789	phoneutria
652	2	5.9	34	1	TXP5_BRASM	P49266	brachypelma
653	2	5.9	34	1	VLYS_BPM1	P08229	bacterioph
654	2	5.9	34	1	VPU_HV1W2	P08808	human immun
655	2	5.9	34	1	Y05J_BPT4	P39239	bacterioph
656	2	5.9	34	1	Y224_TREPA	O83253	treponema p
657	2	5.9	34	1	Y848_BORBU	O51788	borrelia bu
658	2	5.9	34	1	Y870_HAEIN	P44065	haemophilus
659	2	5.9	34	1	Y967_HAEIN	P44086	haemophilus
660	2	5.9	34	1	YC12_GUITH	O78460	guillardia
661	2	5.9	34	1	YC12_ODOSI	P49529	odontella s
662	2	5.9	34	1	YC12_PORPU	P51385	porphyra pu
663	2	5.9	34	1	YC12_SKECO	O96797	skeletonema
664	2	5.9	34	1	YMIA_AGRTU	P38437	agrobacteri
665	2	5.9	34	1	Z33B_HUMAN	Q06731	homo sapien
666	2	5.9	35	1	ADO1_AGRDO	P58608	agriosphodr
667	2	5.9	35	1	C550_BACHA	P80091	bacillus ha
668	2	5.9	35	1	CEC4_BOMMO	P14666	bombyx mori
669	2	5.9	35	1	CECA_HELVI	P83413	heliopsis v
670	2	5.9	35	1	CECB_ANTPE	P01509	antheraea p
671	2	5.9	35	1	CHI1_CASSA	P29137	castanea sa
672	2	5.9	35	1	D3HI_RABIT	P32185	oryctolagus
673	2	5.9	35	1	DEFB_MYTED	P81611	mytilus edu
674	2	5.9	35	1	END4_YEREN	P42691	yersinia en
675	2	5.9	35	1	ERFK_KLEAE	Q08599	klebsiella
676	2	5.9	35	1	EXE2_HELVS	P04204	heloderma s
677	2	5.9	35	1	FAS_CAPHI	P08757	capra hircu
678	2	5.9	35	1	FLAV_NOSSM	P35707	nostoc sp.
679	2	5.9	35	1	GBGU_MOUSE	Q61017	mus musculu
680	2	5.9	35	1	GRDB_CLOPU	P55793	clostridium
681	2	5.9	35	1	GUR_GYMSY	P25810	gymnema syl
682	2	5.9	35	1	HMWC_DESGI	P38588	desulfovibr
683	2	5.9	35	1	IAAC_HORVU	P34951	hordeum vul
684	2	5.9	35	1	KPPR_PINPS	P81664	pinus pinas
685	2	5.9	35	1	LCGB_LACLA	P36962	lactococcus
686	2	5.9	35	1	NEF_HV1H3	P05854	human immun
687	2	5.9	35	1	PBP1_LYMDI	P34176	lymantria d
688	2	5.9	35	1	PBP2_LYMDI	P34177	lymantria d
689	2	5.9	35	1	PBP_HYACE	P34175	hyalophora
690	2	5.9	35	1	PHI1_MYTCA	P35422	mytilus cal
691	2	5.9	35	1	PSAI_CYAPA	P48116	cyanophora
692	2	5.9	35	1	PSBT_MARPO	P12182	marchantia
693	2	5.9	35	1	PSBT_OENHO	P37258	oenothera h
694	2	5.9	35	1	PSBT_ORYSA	P12183	oryza sativ
695	2	5.9	35	1	PSBT_PINTH	P41625	pinus thunb
696	2	5.9	35	1	PSPC_PIG	P15785	sus scrofa
697	2	5.9	35	1	RL32_HALCU	P05965	halobacteri
698	2	5.9	35	1	SCKB_PANIM	P55928	pandinus im
699	2	5.9	35	1	SCKG_PANIM	Q10726	pandinus im
700	2	5.9	35	1	SCX1_BUTSI	P15229	buthus sind
701	2	5.9	35	1	SCX5_BUTEU	P15222	buthus eupe

702	2	5.9	35	1	SCXP_ANDMA	P01498	androctonus
703	2	5.9	35	1	SMS_LAMFL	Q9pr00	lampetra fl
704	2	5.9	35	1	SPRC_PIG	P20112	sus scrofa
705	2	5.9	35	1	THPA_THADA	P21381	thaumatococ
706	2	5.9	35	1	TMTX_MESTA	Q9bn12	mesobuthus
707	2	5.9	35	1	TXAG_AGEOP	P31328	agelena opu
708	2	5.9	35	1	TXH4_SELHU	P83303	selenocosmi
709	2	5.9	35	1	TXKS_STOHE	P29187	stoichactis
710	2	5.9	35	1	TXN4_SELHA	P83471	selenocosmi
711	2	5.9	35	1	VL3_PAPVD	P06919	deer papill
712	2	5.9	35	1	VSPA_CERVI	P18692	cerastes vi
713	2	5.9	35	1	WSP7_PINPS	P81086	pinus pinas
714	2	5.9	35	1	Y320_BORBU	O51299	borrelia bu
715	2	5.9	35	1	Y37_BPT3	P20325	bacterioph
716	2	5.9	35	1	Y644_ARCFU	O29613	archaeoglob
717	2	5.9	35	1	Y845_BORBU	O51785	borrelia bu
718	2	5.9	35	1	Y847_BORBU	O51787	borrelia bu
719	2	5.9	35	1	YC12_CYACA	Q9tlx0	cyanidium c
720	2	5.9	35	1	YC69_ARCFU	O28999	archaeoglob
721	2	5.9	35	1	YQB5_CAEEL	Q09258	caenorhabdi
722	2	5.9	36	1	AMPL_PIG	P28839	sus scrofa
723	2	5.9	36	1	ANFV_ANGJA	P22642	anguilla ja
724	2	5.9	36	1	C3L1_BOVIN	P30922	bos taurus
725	2	5.9	36	1	CBBA_NITVU	P37102	nitrobacter
726	2	5.9	36	1	CECD_ANTPE	P01511	antheraea p
727	2	5.9	36	1	CYC7_GEOME	P81894	geobacter m
728	2	5.9	36	1	DESR_DESGI	P00273	desulfovibr
729	2	5.9	36	1	F4RE_METOG	P80951	methanogeni
730	2	5.9	36	1	GLU1_ORENI	P81026	oreochromis
731	2	5.9	36	1	GLUC_HYDCO	P09682	hydrolagus
732	2	5.9	36	1	H1L5_ENSMI	P27203	ensis minor
733	2	5.9	36	1	HBB_PONPY	Q9tt34	pongo pygma
734	2	5.9	36	1	IAA_STRAU	P04082	streptomyce
735	2	5.9	36	1	IOB1_ISYOB	P58609	isyndus obs
736	2	5.9	36	1	KAD_STRGR	P53398	streptomyce
737	2	5.9	36	1	LHG_RHOVI	P04126	rhodopseudo
738	2	5.9	36	1	LYOX_PIG	P45845	sus scrofa
739	2	5.9	36	1	MFA1_YEAST	P34165	saccharomyc
740	2	5.9	36	1	MPG2_DACGL	Q41183	dactylis gl
741	2	5.9	36	1	MYPC_RAT	P56741	rattus norv
742	2	5.9	36	1	NEUH_CARCA	P11975	cardisoma c
743	2	5.9	36	1	NEUY_GADMO	P80167	gadus morhu
744	2	5.9	36	1	NEUY_ONCMY	P29071	oncorhynch
745	2	5.9	36	1	NEUY_RABIT	P09640	oryctolagus
746	2	5.9	36	1	NEUY_RANRI	P29949	rana ridibu
747	2	5.9	36	1	NIFH_ENTAG	P26249	enterobacte
748	2	5.9	36	1	NLTP_PINPI	P26912	pinus pinea
749	2	5.9	36	1	NUCM_SOLTU	P80264	solanum tub
750	2	5.9	36	1	OST2_CHICK	P80897	gallus gall
751	2	5.9	36	1	PAHO_ALLMI	P06305	alligator m
752	2	5.9	36	1	PAHO_ANSAN	P06304	anser anser
753	2	5.9	36	1	PAHO_CERSI	P37999	ceratotheri
754	2	5.9	36	1	PAHO_DIDMA	P18107	didelphis m
755	2	5.9	36	1	PAHO_EQUZE	P38000	equus zebra
756	2	5.9	36	1	PAHO_ERIEU	P41335	erinaceus e
757	2	5.9	36	1	PAHO_LARAR	P41337	larus argen
758	2	5.9	36	1	PAHO_MACMU	P33684	macaca mula

759	2	5.9	36	1	PAHO_RABIT	P41336	oryctolagus
760	2	5.9	36	1	PAHO_RANCA	P15427	rana catesb
761	2	5.9	36	1	PAHO_RANTE	P31229	rana tempor
762	2	5.9	36	1	PAHO_STRCA	P11967	struthio ca
763	2	5.9	36	1	PAHO_TAPPI	P39659	tapirus pin
764	2	5.9	36	1	PGKH_CHLFU	P36232	chlorella f
765	2	5.9	36	1	PMY_PETMA	P80024	petromyzon
766	2	5.9	36	1	PSAD_PEA	P20117	pisum sativ
767	2	5.9	36	1	PSAH_PEA	P20121	pisum sativ
768	2	5.9	36	1	PSAI_ANGLY	P28251	angiopteris
769	2	5.9	36	1	PSAI_BRAOL	Q31909	brassica ol
770	2	5.9	36	1	PSAI_CARCL	Q9gdv2	carpobrotus
771	2	5.9	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
772	2	5.9	36	1	PSAI_CHLVU	P58214	chlorella v
773	2	5.9	36	1	PSAI_CYACA	Q9tm24	cyanidium c
774	2	5.9	36	1	PSAI_GUITH	O78462	guillardia
775	2	5.9	36	1	PSAI_HORVU	P13165	hordeum vul
776	2	5.9	36	1	PSAI_MAIZE	P30980	zea mays (m
777	2	5.9	36	1	PSAI_MARPO	P12185	marchantia
778	2	5.9	36	1	PSAI_MESVI	Q9muq4	mesostigma
779	2	5.9	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
780	2	5.9	36	1	PSAI_ORYSA	P12186	oryza sativ
781	2	5.9	36	1	PSAI_PICAB	O47040	picea abies
782	2	5.9	36	1	PSAI_PORPU	P51387	porphyra pu
783	2	5.9	36	1	PSAI_PSINU	Q8wi10	psilotum nu
784	2	5.9	36	1	PSAI_SKECO	O96813	skeletonema
785	2	5.9	36	1	PSAI_TOBAC	P12187	nicotiana t
786	2	5.9	36	1	PSAI_WHEAT	P25410	triticum ae
787	2	5.9	36	1	PSBI_ARATH	P09970	arabidopsis
788	2	5.9	36	1	PSBI_HORVU	P25876	hordeum vul
789	2	5.9	36	1	PSBI_MARPO	P09969	marchantia
790	2	5.9	36	1	PSBI_ORYSA	P12161	oryza sativ
791	2	5.9	36	1	PSBI_PINTH	P41599	pinus thunb
792	2	5.9	36	1	PSBI_PSEMZ	P29796	pseudotsuga
793	2	5.9	36	1	PSBM_CHLVU	P56325	chlorella v
794	2	5.9	36	1	PSBM_SYNEL	Q8dha7	synechococc
795	2	5.9	36	1	PSBY_ODOSI	P49543	odontella s
796	2	5.9	36	1	PSBY_PORPU	P51206	porphyra pu
797	2	5.9	36	1	PYY_AMICA	P29205	amia calva
798	2	5.9	36	1	PYY_LEPSP	P09473	lepisosteus
799	2	5.9	36	1	PYY_MYOSC	P09641	myoxocephal
800	2	5.9	36	1	PYY_ONCKI	P09474	oncorhynchu
801	2	5.9	36	1	PYY_ORENI	P81028	oreochromis
802	2	5.9	36	1	PYY_PIG	P01305	sus scrofa
803	2	5.9	36	1	PYY_RAJRH	P29206	raja rhina
804	2	5.9	36	1	PYY_RANRI	P29204	rana ridibu
805	2	5.9	36	1	SCK2_CENLL	P45630	centruroide
806	2	5.9	36	1	SCK3_LEIQH	P45660	leiurus qui
807	2	5.9	36	1	SCX1_BUTEU	P15220	buthus eupe
808	2	5.9	36	1	SCXL_LEIQU	P45639	leiurus qui
809	2	5.9	36	1	SPYY_PHYBI	P80952	phyllomedus
810	2	5.9	36	1	TAEK_ACTEQ	P81897	actinia equ
811	2	5.9	36	1	TERN_PSEUS	P82321	pseudacanth
812	2	5.9	36	1	TLN1_CHICK	P54939	gallus gall
813	2	5.9	36	1	TX1B_AGEAP	P15970	agelenopsis
814	2	5.9	36	1	TX35_PHONI	P81791	phoneutria
815	2	5.9	36	1	TXAM_METSE	P11495	metridium s

816	2	5.9	36	1	TXD3_PARLU	P83258	paracoelote
817	2	5.9	36	1	TXJA_HADVE	P82227	hadronyche
818	2	5.9	36	1	TXJB_HADVE	P82226	hadronyche
819	2	5.9	36	1	Y16L_BPT4	P39244	bacterioph
820	2	5.9	36	1	Y297_ARCFU	O29945	archaeoglob
821	2	5.9	36	1	Y4KD_BPCHP	P19188	bacterioph
822	2	5.9	36	1	Y609_BORBU	O51554	borrelia bu
823	2	5.9	36	1	Y619_ARCFU	O29636	archaeoglob
824	2	5.9	36	1	Y699_TREPA	O83697	treponema p
825	2	5.9	36	1	YC12_CYAPA	P48256	cyanophora
826	2	5.9	36	1	YG50_HAEIN	P44281	haemophilus
827	2	5.9	36	1	YRKG_BACSU	P54434	bacillus su
828	2	5.9	37	1	24KD_PLACH	P14592	plasmodium
829	2	5.9	37	1	AFP4_MALPA	P83138	malva parvi
830	2	5.9	37	1	ANP3_PSEAM	P02733	pseudopleur
831	2	5.9	37	1	ATPO_SOLTU	P80504	solanum tub
832	2	5.9	37	1	B2MG_ORENI	Q03423	oreochromis
833	2	5.9	37	1	CAL1_PIG	P30880	sus scrofa
834	2	5.9	37	1	CAL1_SHEEP	P30881	ovis aries
835	2	5.9	37	1	CALR_RANRI	P31888	rana ridibu
836	2	5.9	37	1	CEC2_MANSE	P14662	manduca sex
837	2	5.9	37	1	CEC3_MANSE	P14663	manduca sex
838	2	5.9	37	1	CEC4_MANSE	P14664	manduca sex
839	2	5.9	37	1	CG2S_LUPAN	P09930	lupinus ang
840	2	5.9	37	1	CHCD_ANTPO	P08931	antheraea p
841	2	5.9	37	1	CS40_STAAU	P81684	staphylococ
842	2	5.9	37	1	CUP4_SARBU	P14486	sarcophaga
843	2	5.9	37	1	DEFA_MYTED	P81610	mytilus edu
844	2	5.9	37	1	ECAA_ECTTU	P49343	ectatomma t
845	2	5.9	37	1	ES2A_RANES	P40845	rana escule
846	2	5.9	37	1	ES2B_RANES	P40846	rana escule
847	2	5.9	37	1	F13A_BOVIN	P12260	bos taurus
848	2	5.9	37	1	GHR3_RAT	P33580	rattus norv
849	2	5.9	37	1	HCYB_CANPG	P83175	cancer pagu
850	2	5.9	37	1	HOXF_RHOOP	P22658	rhodococcus
851	2	5.9	37	1	LPPY_SERMA	P19937	serratia ma
852	2	5.9	37	1	MAUR_PARVE	Q56462	paracoccus
853	2	5.9	37	1	ME20_EUPRA	P26888	euplotes ra
854	2	5.9	37	1	ME22_EUPRA	P58548	euplotes ra
855	2	5.9	37	1	MIBP_PSESP	P04576	pseudomonas
856	2	5.9	37	1	NLT3_VITSX	P80273	vitis sp. (
857	2	5.9	37	1	NLT4_VITSX	P80274	vitis sp. (
858	2	5.9	37	1	NUFM_SOLTU	P80266	solanum tub
859	2	5.9	37	1	OP2A_OXYKI	P83248	oxyopes kit
860	2	5.9	37	1	OP2B_OXYKI	P83249	oxyopes kit
861	2	5.9	37	1	OP2C_OXYKI	P83250	oxyopes kit
862	2	5.9	37	1	OP2D_OXYKI	P83251	oxyopes kit
863	2	5.9	37	1	PETG_ANASP	P58246	anabaena sp
864	2	5.9	37	1	PETG_ANAVA	Q913p7	anabaena va
865	2	5.9	37	1	PETG_ARATH	P56775	arabidopsis
866	2	5.9	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
867	2	5.9	37	1	PETG_CHLEU	P46304	chlamydomon
868	2	5.9	37	1	PETG_CHLRE	Q08362	chlamydomon
869	2	5.9	37	1	PETG_CHLVU	P56305	chlorella v
870	2	5.9	37	1	PETG_CUSRE	P30398	cuscuta ref
871	2	5.9	37	1	PETG_CYAPA	P14236	cyanophora
872	2	5.9	37	1	PETG_EUGGR	P30396	euglena gra

873	2	5.9	37	1	PETG_GUITH	O78505	guillardia
874	2	5.9	37	1	PETG_MARPO	P12120	marchantia
875	2	5.9	37	1	PETG_MESVI	Q9mun3	mesostigma
876	2	5.9	37	1	PETG_NEPOL	Q9tky8	nephroselmi
877	2	5.9	37	1	PETG_ODOSI	P49470	odontella s
878	2	5.9	37	1	PETG_ORYSA	P12121	oryza sativ
879	2	5.9	37	1	PETG_PINTH	P41614	pinus thunb
880	2	5.9	37	1	PETG_PORPU	P51318	porphyra pu
881	2	5.9	37	1	PETG_PSINU	Q8wi02	psilotum nu
882	2	5.9	37	1	PETG_SKECO	O96811	skeletonema
883	2	5.9	37	1	PETG_SYNEL	Q8dki2	synechococc
884	2	5.9	37	1	PETG_SYNP7	Q9z3g1	synechococc
885	2	5.9	37	1	PIIL_ACHLY	P81720	achromobact
886	2	5.9	37	1	POLN_WEEV	P13896	western equ
887	2	5.9	37	1	PRF1_RAT	P18889	rattus norv
888	2	5.9	37	1	PSAI_ARATH	P56768	arabidopsis
889	2	5.9	37	1	PSAJ_EUGGR	P30394	euglena gra
890	2	5.9	37	1	PSBL_ARATH	P29301	arabidopsis
891	2	5.9	37	1	PSBL_ORYSA	P12166	oryza sativ
892	2	5.9	37	1	PSBM_PINTH	P41608	pinus thunb
893	2	5.9	37	1	PSBY_CYACA	O19893	cyanidium c
894	2	5.9	37	1	PSBY_GUITH	O78433	guillardia
895	2	5.9	37	1	PYY_CHICK	P29203	gallus gall
896	2	5.9	37	1	REV_SIVM2	P08809	simian immu
897	2	5.9	37	1	RK36_ARATH	P12144	arabidopsis
898	2	5.9	37	1	RK36_ASTLO	P24355	astasia lon
899	2	5.9	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
900	2	5.9	37	1	RK36_CHLVU	P56360	chlorella v
901	2	5.9	37	1	RK36_CYACA	Q9tlu9	cyanidium c
902	2	5.9	37	1	RK36_CYAPA	P48131	cyanophora
903	2	5.9	37	1	RK36_EPIVI	P30069	epifagus vi
904	2	5.9	37	1	RK36_EUGGR	P21532	euglena gra
905	2	5.9	37	1	RK36_LOTJA	Q9bbq2	lotus japon
906	2	5.9	37	1	RK36_MARPO	P12142	marchantia
907	2	5.9	37	1	RK36_NEPOL	Q9tl26	nephroselmi
908	2	5.9	37	1	RK36_ODOSI	P49568	odontella s
909	2	5.9	37	1	RK36_OENHO	Q9mtj1	oenothera h
910	2	5.9	37	1	RK36_ORYSA	P12143	oryza sativ
911	2	5.9	37	1	RK36_PEA	P07815	pisum sativ
912	2	5.9	37	1	RK36_PINTH	P41631	pinus thunb
913	2	5.9	37	1	RK36_PORPU	P51296	porphyra pu
914	2	5.9	37	1	RK36_PSINU	Q8why9	psilotum nu
915	2	5.9	37	1	RK36_SPIOL	P12230	spinacia ol
916	2	5.9	37	1	RL36_ANASP	Q8ypk0	anabaena sp
917	2	5.9	37	1	RL36_AQUAE	O66487	aquifex aeo
918	2	5.9	37	1	RL36_BACHD	O50631	bacillus ha
919	2	5.9	37	1	RL36_BACST	P07841	bacillus st
920	2	5.9	37	1	RL36_BACSU	P20278	bacillus su
921	2	5.9	37	1	RL36_BORBU	O51452	borrelia bu
922	2	5.9	37	1	RL36_CAMJE	Q9pm84	campylobact
923	2	5.9	37	1	RL36_CLOAB	Q97ek2	clostridium
924	2	5.9	37	1	RL36_CLOPE	Q8xhu7	clostridium
925	2	5.9	37	1	RL36_DEIRA	Q9rsk0	deinococcus
926	2	5.9	37	1	RL36_HAEIN	P46361	haemophilus
927	2	5.9	37	1	RL36_HELPJ	Q9zjt1	helicobacte
928	2	5.9	37	1	RL36_HELPY	P56058	helicobacte
929	2	5.9	37	1	RL36_LEPIN	Q9xd13	leptospira

930	2	5.9	37	1	RL36_LISMO	Q927n0	listeria mo
931	2	5.9	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
932	2	5.9	37	1	RL36_MYCGE	P47420	mycoplasma
933	2	5.9	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
934	2	5.9	37	1	RL36_MYCPN	P52864	mycoplasma
935	2	5.9	37	1	RL36_MYCPU	Q98q05	mycoplasma
936	2	5.9	37	1	RL36_MYCSP	P38015	mycoplasma
937	2	5.9	37	1	RL36_MYCTU	P45810	mycobacteri
938	2	5.9	37	1	RL36_NEIMA	Q9jrb2	neisseria m
939	2	5.9	37	1	RL36_STAAM	Q99s42	staphylococ
940	2	5.9	37	1	RL36_STRCO	O86772	streptomyce
941	2	5.9	37	1	RL36_SYNP6	O24707	synechococc
942	2	5.9	37	1	RL36_THETH	P80256	thermus the
943	2	5.9	37	1	RL36_THETN	Q8r7x8	thermoanaer
944	2	5.9	37	1	RL36_TREPA	O83239	treponema p
945	2	5.9	37	1	RL36_UREPA	Q9pqn7	ureaplasma
946	2	5.9	37	1	RL36_VIBCH	P78001	vibrio chol
947	2	5.9	37	1	RL7_CLOPA	P05393	clostridium
948	2	5.9	37	1	RS15_HELLU	P52820	helix lucor
949	2	5.9	37	1	RUGC_RANRU	P80956	rana rugosa
950	2	5.9	37	1	SCIT_MESTA	P81761	mesobuthus
951	2	5.9	37	1	SCK2_LEIQH	P45628	leiurus qui
952	2	5.9	37	1	SCK3_BUTOC	P59290	buthus occi
953	2	5.9	37	1	SCK3_PARTR	P83112	parabuthus
954	2	5.9	37	1	SCKA_TITSE	P46114	tityus serr
955	2	5.9	37	1	SCKC_LEIQH	P13487	leiurus qui
956	2	5.9	37	1	SMS_PETMA	P21779	petromyzon
957	2	5.9	37	1	TCTP_TRYBB	P35758	trypanosoma
958	2	5.9	37	1	THHS_HORVU	P33045	hordeum vul
959	2	5.9	37	1	TX21_SELHU	P82959	selenocosmi
960	2	5.9	37	1	TX22_SELHU	P82960	selenocosmi
961	2	5.9	37	1	TXD1_PARLU	P83256	paracoelote
962	2	5.9	37	1	TXD2_PARLU	P83257	paracoelote
963	2	5.9	37	1	TXD4_PARLU	P83259	paracoelote
964	2	5.9	37	1	TXJC_HADVE	P82228	hadronyche
965	2	5.9	37	1	TXKB_BUNGR	P29186	bunodosoma
966	2	5.9	37	1	TXOF_HADVE	P81599	hadronyche
967	2	5.9	37	1	TXP3_APTSC	P49268	aptostichus
968	2	5.9	37	1	VA1_BPBF2	P19347	bacterioph
969	2	5.9	37	1	VG40_BPML5	Q05250	mycobacteri
970	2	5.9	37	1	VG65_BPPH2	P16515	bacterioph
971	2	5.9	37	1	VG65_BPPZA	P08384	bacterioph
972	2	5.9	37	1	VGJ_BPPHX	P03651	bacterioph
973	2	5.9	37	1	VP64_NPVBM	P41722	bombyx mori
974	2	5.9	37	1	VPU_HV1Z8	P08807	human immun
975	2	5.9	37	1	Y268_ARCFU	O29971	archaeoglob
976	2	5.9	37	1	Y63_BPT7	P03799	bacterioph
977	2	5.9	37	1	Y692_BORBU	O51635	borrelia bu
978	2	5.9	37	1	Y700_BORBU	O51643	borrelia bu
979	2	5.9	37	1	Y762_BORBU	O51703	borrelia bu
980	2	5.9	37	1	Y846_BORBU	O51786	borrelia bu
981	2	5.9	37	1	YBGT_ECOLI	P56100	escherichia
982	2	5.9	37	1	YC12_CHLVU	P56328	chlorella v
983	2	5.9	37	1	YDA3_SCHPO	Q10345	schizosacch
984	2	5.9	37	1	YIM4_BPPH1	P10428	bacterioph
985	2	5.9	37	1	YQGE_BACCA	P28753	bacillus ca
986	2	5.9	37	1	YRYL_CAEEL	Q19177	caenorhabdi



987	2	5.9	38	1	A2M_HOMAM	P20737 homarus ame
988	2	5.9	38	1	AFP5_MALPA	P83139 malva parvi
989	2	5.9	38	1	BD01_BOVIN	P46159 bos taurus
990	2	5.9	38	1	BD08_BOVIN	P46166 bos taurus
991	2	5.9	38	1	COA3_XANCP	Q07484 xanthomonas
992	2	5.9	38	1	CRS3_NOTGO	P15534 nototodarus
993	2	5.9	38	1	CU47_LACCU	P80323 lactobacill
994	2	5.9	38	1	DCHS_MICSP	P00863 micrococcus
995	2	5.9	38	1	DEF4_LEIQH	P41965 leiurus qui
996	2	5.9	38	1	DEF7_SPIOL	P81573 spinacia ol
997	2	5.9	38	1	DEFI_AESCY	P80154 aeschna cya
998	2	5.9	38	1	DEFI_MYTGA	P80571 mytilus gal
999	2	5.9	38	1	DLP3_ORNAN	P82141 ornithorhyn
1000	2	5.9	38	1	DPOB_BOVIN	Q27958 bos taurus

# ALIGNMENTS

## RESULT 1

### FABI\_RHASA

ID FABI\_RHASA STANDARD; PRT; 33 AA.

AC P81175;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).

OS Rhamdia sapo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Pimelodidae; Rhamdia.

OX NCBI\_TaxID=55673;

RN [1]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=98036128; PubMed=9370361;

RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,

RA Santome J.A.;

RT "Amino acid sequence, binding properties and evolutionary

RT relationships of the basic liver fatty-acid-binding protein from the

RT catfish Rhamdia sapo.";

RL Eur. J. Biochem. 249:510-517(1997).

CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: INTESTINE.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

DR InterPro; IPR000463; Fatty\_acid\_BP.

DR PROSITE; PS00214; FABP; PARTIAL.

KW Transport; Lipid-binding.

FT NON\_TER 1 1

FT NON\_CONS 12 13

FT NON\_CONS 20 21

FT NON\_CONS 28 29

FT NON\_TER 33 33

SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 14.7%; Score 5; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5  
|||||  
Db 13 SVSEI 17

RESULT 2

DMD\_RAT

ID DMD\_RAT STANDARD; PRT; 29 AA.  
AC P11530;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Dystrophin (Fragment).  
GN DMD.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88122671; PubMed=3340214;  
RA Nudel U., Robzyk K., Yaffe D.;  
RT "Expression of the putative Duchenne muscular dystrophy gene in  
RT differentiated myogenic cell cultures and in the brain.";  
RL Nature 331:635-638(1988).  
CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the  
CC plasma membrane.  
CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1  
CC and SNTG2 (By similarity).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X07000; CAA30057.1; -.  
DR PIR; S01614; S01614.  
DR InterPro; IPR001589; Actbind\_actnin.  
DR InterPro; IPR001202; WW\_Rsp5\_WWP.  
DR PROSITE; PS00019; ACTININ\_1; PARTIAL.  
DR PROSITE; PS00020; ACTININ\_2; PARTIAL.  
DR PROSITE; PS01159; WW\_DOMAIN\_1; PARTIAL.  
DR PROSITE; PS50020; WW\_DOMAIN\_2; PARTIAL.  
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;  
KW Repeat.  
FT NON\_TER 1 1  
FT NON\_TER 29 29  
SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30  
|||  
Db 12 KLQD 15

RESULT 3

PSBY\_SYNY3

ID PSBY\_SYNY3 STANDARD; PRT; 39 AA.  
AC P73676;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Photosystem II protein Y.  
GN PSBY OR SML0007.  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97061201; PubMed=8905231;  
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,  
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
RA Tabata S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
CC -!- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE  
CC METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM  
CC II (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CELLULAR THYLAKOID MEMBRANE.  
CC -!- SIMILARITY: BELONGS TO THE PSBY FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; D90908; BAA17722.1; -.  
DR PIR; S77164; S77164.  
KW Photosystem II; Transmembrane; Thylakoid; Complete proteome.  
FT TRANSMEM 5 25 POTENTIAL.  
SQ SEQUENCE 39 AA; 4202 MW; 3EA176ABAA79F6DF CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31  
 ||||  
 Db 31 LQDV 34

# RESULT 4

## SR1C\_SARPE

ID SR1C\_SARPE STANDARD; PRT; 39 AA.  
 AC P08377;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Sarcotoxin IC.  
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7386;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85207747; PubMed=3888997;  
 RA Okada M., Natori S.;  
 RT "Primary structure of sarcotoxin I, an antibacterial protein induced  
 RT in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.";  
 RL J. Biol. Chem. 260:7174-7177(1985).  
 CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,  
 CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH  
 CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.  
 DR PIR; C22625; CKFHCS.  
 DR InterPro; IPR000875; Cecropin.  
 DR InterPro; IPR003253; Sarctxn\_cecrpn.  
 DR Pfam; PF00272; cecropin; 1.  
 DR ProDom; PD001670; Sarctxn\_cecrpn; 1.  
 DR PROSITE; PS00268; CECROPIN; 1.  
 KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.  
 FT MOD\_RES 39 39 AMIDATION.  
 SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26  
 ||||  
 Db 2 WLRK 5

# RESULT 5

## CH60\_MYCSM

ID CH60\_MYCSM STANDARD; PRT; 28 AA.  
 AC P80673;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).

GN GROL OR GROEL OR MOPA.  
 OS Mycobacterium smegmatis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1772;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;  
 RX MEDLINE=97387814; PubMed=9243799;  
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;  
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein  
 RT expression in iron-starved Mycobacterium smegmatis."  
 RL BioMetals 10:215-225(1997).  
 CC !- FUNCTION: Prevents misfolding and promotes the refolding and  
 CC proper assembly of unfolded polypeptides generated under stress  
 CC conditions.  
 CC !- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of  
 CC 7 subunits (By similarity).  
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC !- SIMILARITY: Belongs to the chaperonin (HSP60) family.  
 DR HAMAP; MF\_00600; -; 1.  
 DR InterPro; IPR001844; Chaperonin\_Cpn60.  
 DR PROSITE; PS00296; CHAPERONINS\_CPN60; PARTIAL.  
 KW Chaperone; ATP-binding.  
 FT NON\_TER 28 28  
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
 |||  
 Db 18 LNS 20

#### RESULT 6

##### COXB\_SOLTU

ID COXB\_SOLTU STANDARD; PRT; 28 AA.  
 AC P80499;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Tuber;  
 RX MEDLINE=97077345; PubMed=8919912;  
 RA Jansch L., Kruff V., Schmitz U.K., Braun H.P.;  
 RT "New insights into the composition, molecular mass and stoichiometry  
 RT of the protein complexes of plant mitochondria."  
 RL Plant J. 9:357-368(1996).

CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.  
 DR InterPro; IPR002124; COX5B.  
 DR PROSITE; PS00848; COX5B; PARTIAL.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 28 28  
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4  
 |||  
 Db 2 VSE 4

#### RESULT 7

GUN\_SCHCO  
 ID GUN\_SCHCO STANDARD; PRT; 28 AA.  
 AC P81190;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)  
 DE (Fragment).  
 OS Schizophyllum commune (Bracket fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Agaricales; Schizophyllaceae; Schizophyllum.  
 OX NCBI\_TaxID=5334;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=97459758; PubMed=9315718;  
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;  
 RT "Identification of the catalytic nucleophile in the cellulase from  
 RT Schizophyllum commune and assignment of the enzyme to Family 5,  
 RT subtype 5 of the glycosidases."  
 RL FEBS Lett. 414:359-361(1997).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 CC (Probable).  
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL  
 CC HYDROLASES).  
 DR InterPro; IPR001547; Glyco\_hydro\_5.  
 DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; PARTIAL.  
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;  
 KW Lipoprotein.  
 FT ACT\_SITE 20 20 NUCLEOPHILE.  
 FT NON\_TER 28 28  
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24  
|||  
Db 7 EWL 9

RESULT 8

PA23\_TRIST

ID PA23\_TRIST STANDARD; PRT; 28 AA.  
AC P82894;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)  
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).  
OS Trimeresurus stejnegeri (Chinese green tree viper).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCBI\_TaxID=39682;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Li S.Y., Wang W.Y., Xiong Y.L.;  
RT "Isolation, sequence and characterization of five variants of  
RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";  
RL Submitted (DEC-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic  
CC activities are not detected.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II  
CC SUBFAMILY.  
DR HSSP; P82287; 1QLL.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR PROSITE; PS00119; PA2\_ASP; PARTIAL.  
DR PROSITE; PS00118; PA2\_HIS; PARTIAL.  
KW Hydrolase; Lipid degradation; Calcium; Multigene family.  
FT NON\_TER 28 28  
SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13  
|||  
Db 5 LGK 7

RESULT 9

PA2C\_PSEPO

ID PA2C\_PSEPO STANDARD; PRT; 28 AA.  
AC P20260;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine  
DE 2-acylhydrolase) (Fragment).  
OS Pseudechis porphyriacus (Red-bellied black snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudechis.  
OX NCBI\_TaxID=8671;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=89388835; PubMed=2675391;  
RA Schmidt J.J., Middlebrook J.L.;  
RT "Purification, sequencing and characterization of pseudexin  
RT phospholipases A2 from Pseudechis porphyriacus (Australian  
RT red-bellied black snake).";  
RL Toxicon 27:805-818(1989).  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
CC acyl groups in 3-sn-phosphoglycerides.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I  
CC SUBFAMILY.  
DR PIR; C32416; C32416.  
DR HSSP; P00592; 2PHI.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR PROSITE; PS00119; PA2\_ASP; PARTIAL.  
DR PROSITE; PS00118; PA2\_HIS; PARTIAL.  
KW Hydrolase; Lipid degradation; Calcium; Multigene family.  
FT NON\_TER 28 28  
SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAA0D5 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7  
|||  
Db 3 IQL 5

# RESULT 10

## VI03\_VACCP

ID VI03\_VACCP STANDARD; PRT; 28 AA.  
AC Q00334;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Protein I3 (Fragment).



GN I3L.  
 OS Vaccinia virus (strain L-IVP).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=31531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91066899; PubMed=2250685;  
 RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,  
 RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,  
 RA Malygin E.G.;  
 RT "Molecular-biological study of vaccinia virus genome. II.  
 RT Localization and nucleotide sequence of vaccinia virus genes coding  
 RT for proteins 36K and 12K.";  
 RL Mol. Biol. (Mosk) 24:968-976(1990).  
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS  
 CC THE LATE PHASE OF INFECTION.  
 CC -----  
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 CC -----  
 DR EMBL; X61165; CAA43473.1; -.  
 DR InterPro; IPR006754; Pox\_I3.  
 DR Pfam; PF04661; Pox\_I3; 1.  
 KW Early protein; Late protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12  
 |||  
 Db 5 NLG 7

# RESULT 11

## VIP\_ALLMI

ID VIP\_ALLMI STANDARD; PRT; 28 AA.  
 AC P48142; P01285;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Vasoactive intestinal peptide (VIP).  
 GN VIP.  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Stomach;  
 RX MEDLINE=93324451; PubMed=8101369;  
 RA Wang Y., Conlon J.M.;  
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain  
 RT and stomach of the alligator.";  
 RL Peptides 14:573-579(1993).  
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD  
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES  
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH  
 CC AND GALL BLADDER.  
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 1.  
 DR PRINTS; PR00275; GLUCAGON.  
 DR SMART; SM00070; GLUCA; 1.  
 DR PROSITE; PS00260; GLUCAGON; 1.  
 KW Glucagon family; Amidation; Hormone.  
 FT MOD\_RES 28 28 AMIDATION.  
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
 |||  
 Db 23 LNS 25

# RESULT 12

## VIP\_RANRI

ID VIP\_RANRI STANDARD; PRT; 28 AA.  
 AC P81016;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Vasoactive intestinal peptide (VIP).  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95309202; PubMed=7540547;  
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;  
 RT "Frog vasoactive intestinal polypeptide and galanin: primary  
 RT structures and effects on pituitary adenylate cyclase.";  
 RL Endocrinology 136:3079-3086(1995).  
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD  
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES  
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH  
 CC AND GALL BLADDER.  
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 1.  
 DR PRINTS; PR00275; GLUCAGON.  
 DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Amidation; Hormone.  
FT MOD\_RES 28 28 AMIDATION.  
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 23 LNS 25

# RESULT 13

## VIP\_SHEEP

ID VIP\_SHEEP STANDARD; PRT; 28 AA.  
AC P04565;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Vasoactive intestinal peptide (VIP).  
GN VIP.  
OS Ovis aries (Sheep),  
OS Capra hircus (Goat), and  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940, 9925, 9615;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Sheep; TISSUE=Brain;  
RX MEDLINE=91045331; PubMed=2235680;  
RA Gafvelin G.;  
RT "Isolation and primary structure of VIP from sheep brain."  
RL Peptides 11:703-706(1990).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=Sheep; TISSUE=Small intestine;  
RX MEDLINE=91239834; PubMed=2034821;  
RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,  
RA Christophe J.;  
RT "Purification and amino acid sequence of vasoactive intestinal  
RT peptide, peptide histidine isoleucinamide and secretin from the ovine  
RT small intestine."  
RL Regul. Pept. 32:169-179(1991).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=C.hircus, and C.familiaris;  
RX MEDLINE=86313167; PubMed=3748846;  
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;  
RT "Purification and amino acid sequences of dog, goat and guinea pig  
RT VIPs."  
RL Peptides 7 Suppl. 1:17-20(1986).  
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD  
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES  
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH

CC AND GALL BLADDER.  
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR PIR; A60304; A60304.  
 DR PIR; B60072; VRSH.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 1.  
 DR PRINTS; PR00275; GLUCAGON.  
 DR SMART; SM00070; GLUCA; 1.  
 DR PROSITE; PS00260; GLUCAGON; 1.  
 KW Glucagon family; Amidation; Hormone.  
 FT MOD\_RES 28 28 AMIDATION.  
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
 |||  
 Db 23 LNS 25

#### RESULT 14

##### GALA\_ALLMI

ID GALA\_ALLMI STANDARD; PRT; 29 AA.  
 AC P47215;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Galanin.  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Stomach;  
 RX MEDLINE=95023390; PubMed=7524049;  
 RA Wang Y., Conlon J.M.;  
 RT "Purification and primary structure of galanin from the alligator  
 RT stomach."  
 RL Peptides 15:603-606(1994).  
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND  
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES  
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL  
 CC SECRETION.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.  
 DR InterPro; IPR001600; Galanin.  
 DR Pfam; PF01296; Galanin; 1.  
 DR ProDom; PD005962; Galanin; 1.  
 DR PROSITE; PS00861; GALANIN; 1.  
 KW Hormone; Neuropeptide; Amidation.  
 FT MOD\_RES 29 29 AMIDATION.  
 SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 4 LNS 6

RESULT 15

GALA\_AMICA

ID GALA\_AMICA STANDARD; PRT; 29 AA.  
AC P47214;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Galanin.  
OS Amia calva (Bowfin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.  
OX NCBI\_TaxID=7924;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Stomach;  
RX MEDLINE=95083480; PubMed=7527531;  
RA Wang Y., Conlon J.M.;  
RT "Purification and characterization of galanin from the  
RT phylogenetically ancient fish, the bowfin (Amia calva) and dogfish  
RT (Scyliorhinus canicula).";  
RL Peptides 15:981-986(1994).  
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND  
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES  
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL  
CC SECRETION.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.  
DR InterPro; IPR001600; Galanin.  
DR Pfam; PF01296; Galanin; 1.  
DR ProDom; PD005962; Galanin; 1.  
DR PROSITE; PS00861; GALANIN; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT MOD\_RES 29 29 AMIDATION.  
SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 4 LNS 6

RESULT 16

GALA\_CHICK

ID GALA\_CHICK STANDARD; PRT; 29 AA.  
AC P30802;  
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Galanin.  
 GN GAL OR GALN  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=91348254; PubMed=1715289;  
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;  
 RT "Chemical detection of natural peptides by specific structures.  
 RT Isolation of chicken galanin by monitoring for its N-terminal  
 RT dipeptide, and determination of the amino acid sequence.";  
 RL FEBS Lett. 288:151-153(1991).  
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND  
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES  
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL  
 CC SECRETION.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.  
 DR PIR; S17147; S17147.  
 DR InterPro; IPR001600; Galanin.  
 DR Pfam; PF01296; Galanin; 1.  
 DR PRINTS; PR00273; GALANIN.  
 DR ProDom; PD005962; Galanin; 1.  
 DR PROSITE; PS00861; GALANIN; 1.  
 KW Hormone; Neuropeptide; Amidation.  
 FT MOD\_RES 29 29 AMIDATION.  
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17  
 |||  
 Db 4 LNS 6

#### RESULT 17

##### GALA\_ONCMY

ID GALA\_ONCMY STANDARD; PRT; 29 AA.  
 AC P47213;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Galanin.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]

RP SEQUENCE.  
RC TISSUE=Stomach;  
RX MEDLINE=95164756; PubMed=7532194;  
RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;  
RT "Characterization of trout galanin and its distribution in trout  
RT brain and pituitary.";  
RL J. Comp. Neurol. 350:63-74(1994).  
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND  
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES  
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL  
CC SECRETION.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.  
DR InterPro; IPR001600; Galanin.  
DR Pfam; PF01296; Galanin; 1.  
DR ProDom; PD005962; Galanin; 1.  
DR PROSITE; PS00861; GALANIN; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT MOD\_RES 29 29 AMIDATION.  
SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 4 LNS 6

# RESULT 18

## GALA\_RANRI

ID GALA\_RANRI STANDARD; PRT; 29 AA.  
AC P47216;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Galanin.  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8406;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95309202; PubMed=7540547;  
RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;  
RT "Frog vasoactive intestinal polypeptide and galanin: primary  
RT structures and effects on pituitary adenylate cyclase.";  
RL Endocrinology 136:3079-3086(1995).  
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND  
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES  
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL  
CC SECRETION.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.  
DR InterPro; IPR001600; Galanin.  
DR Pfam; PF01296; Galanin; 1.

DR ProDom; PD005962; Galanin; 1.  
DR PROSITE; PS00861; GALANIN; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT MOD\_RES 29 29 AMIDATION.  
SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||  
Db 4 LNS 6

#### RESULT 19

##### GALA\_SHEEP

ID GALA\_SHEEP STANDARD; PRT; 29 AA.  
AC P31234;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Galanin.  
GN GAL OR GALN OR GLNN.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92158824; PubMed=1724081;  
RA Sillard R., Langel U., Joernvall H.;  
RT "Isolation and characterization of galanin from sheep brain."  
RL Peptides 12:855-859(1991).  
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND  
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES  
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL  
CC SECRETION.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.  
DR InterPro; IPR001600; Galanin.  
DR Pfam; PF01296; Galanin; 1.  
DR PRINTS; PR00273; GALANIN.  
DR ProDom; PD005962; Galanin; 1.  
DR PROSITE; PS00861; GALANIN; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT MOD\_RES 29 29 AMIDATION.  
SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
|||



Db 4 LNS 6

RESULT 20

GLUC\_CHIBR

ID GLUC\_CHIBR STANDARD; PRT; 29 AA.  
AC P31297;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glucagon.  
GN GCG.  
OS Chinchilla brevicaudata (Chinchilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;  
OC Chinchilla.  
OX NCBI\_TaxID=10152;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91045327; PubMed=2235678;  
RA Eng J., Kleinman W.A., Chu L.S.;  
RT "Purification of peptide hormones from chinchilla pancreas by  
RT chemical assay.";  
RL Peptides 11:683-685(1990).  
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
CC THE BLOOD SUGAR LEVEL.  
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
DR PIR; A60413; GCCB.  
DR HSSP; P01275; 1BH0.  
DR InterPro; IPR000532; Glucagon.  
DR Pfam; PF00123; hormone2; 1.  
DR PRINTS; PR00275; GLUCAGON.  
DR SMART; SM00070; GLUCA; 1.  
DR PROSITE; PS00260; GLUCAGON; 1.  
KW Glucagon family; Hormone.  
SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15  
|||  
Db 12 KHL 14

RESULT 21

IPYR\_DESVH

ID IPYR\_DESVH STANDARD; PRT; 29 AA.  
AC P19371;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-  
DE hydrolase) (PPase) (Fragment).

OS Desulfovibrio vulgaris (strain Hildenborough).  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
 OC Desulfovibrionaceae; Desulfovibrio.  
 OX NCBI\_TaxID=882;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90365722; PubMed=2168174;  
 RA Liu M.-Y., le Gall J.;  
 RT "Purification and characterization of two proteins with inorganic  
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin  
 RT and a new, highly active, enzyme."  
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).  
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE  
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH  
 CC ACTIVITY PYROPHOSPHATASE.  
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.  
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).  
 DR PIR; A35687; A35687.  
 DR HAMAP; MF\_00209; -; 1.  
 DR InterPro; IPR001596; Pyrophosphatase.  
 DR PROSITE; PS00387; PPASE; PARTIAL.  
 KW Hydrolase; Periplasmic.  
 FT NON\_TER 29 29  
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEI 5  
 |||  
 Db 15 SEI 17

## RESULT 22

### NUO1\_SOLTU

ID NUO1\_SOLTU STANDARD; PRT; 29 AA.  
 AC P80267;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Bintje; TISSUE=Tuber;  
 RX MEDLINE=94124587; PubMed=8294484;  
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,  
 RA Grohmann L.;  
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of  
 RT the respiratory chain from the inner mitochondrial membrane of  
 RT Solanum tuberosum.";

RL J. Biol. Chem. 269:2263-2269(1994).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER  
 CC MEMBRANE.  
 DR PIR; I49732; I49732.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 FT NON\_TER 29 29  
 SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKK 27  
 |||  
 Db 2 RKK 4

#### RESULT 23

##### P2SM\_LOXIN

ID P2SM\_LOXIN STANDARD; PRT; 29 AA.  
 AC P83046;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).  
 OS Loxosceles intermedia (Spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.  
 OX NCBI\_TaxID=58218;  
 RN [1]  
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR  
 RP LOCATION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99009277; PubMed=9790962;  
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,  
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;  
 RT "Sphingomyelinases in the venom of the spider Loxosceles intermedia  
 RT are responsible for both dermonecrosis and complement-dependent  
 RT hemolysis."  
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).  
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-  
 CC dependent hemolysis and dermonecrosis.  
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +  
 CC choline phosphate.  
 CC -!- COFACTOR: Calcium ion.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 KW Hydrolase; Toxin; Calcium; Hemolysis.  
 FT NON\_TER 29 29  
 SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12  
|||  
Db 25 NLG 27

RESULT 24

PCG4\_PACGO

ID PCG4\_PACGO STANDARD; PRT; 29 AA.  
AC P82417;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ponericin G4.  
OS Pachycondyla goeldii (Ponerine ant).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;  
OC Ponerinae; Pachycondyla.  
OX NCBI\_TaxID=118888;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Venom;  
RX MEDLINE=21264562; PubMed=11279030;  
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,  
RA Longeon A., Chafotte A., Dejean A., Rossier J.;  
RT "Ponericins, new antibacterial and insecticidal peptides from the  
RT venom of the ant Pachycondyla goeldii.";  
RL J. Biol. Chem. 276:17823-17829(2001).  
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA  
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.  
KW Antibiotic; Insect immunity; Fungicide.  
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24  
|||  
Db 11 EWL 13

RESULT 25

RS7\_METTE

ID RS7\_METTE STANDARD; PRT; 29 AA.  
AC O93639;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 30S ribosomal protein S7P (Fragment).  
GN RPS7P OR S7.  
OS Methanosarcina thermophila.

OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 1825 / TM-1;  
 RX MEDLINE=99059471; PubMed=9845338;  
 RA Thomas T., Cavicchioli R.;  
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis  
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and  
 RT thermophilic methanogens.";  
 RL FEBS Lett. 439:281-287(1998).  
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds  
 CC directly to 16S rRNA where it nucleates assembly of the head  
 CC domain of the 30S subunit. Is located at the subunit interface  
 CC close to the decoding center (By similarity).  
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.  
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF026165; AAC79199.1; -.  
 DR PIR; T44245; T44245.  
 DR HAMAP; MF\_00480; -; 1.  
 DR InterPro; IPR000235; Ribosomal\_S7.  
 DR PROSITE; PS00052; RIBOSOMAL\_S7; PARTIAL.  
 KW Ribosomal protein; RNA-binding; rRNA-binding.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21  
 |||  
 Db 22 ERV 24

#### RESULT 26

SODC\_OLEEU

ID SODC\_OLEEU STANDARD; PRT; 29 AA.

AC P80740;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e  
 DE V) (Fragment).

OS Olea europaea (Common olive).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.  
 OX NCBI\_TaxID=4146;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pollen;  
 RX MEDLINE=98160390; PubMed=9500754;  
 RA Boluda L., Alonso C., Fernandez-Caldas E.;  
 RT "Purification, characterization, and partial sequencing of two new  
 RT allergens of Olea europaea.";  
 RL J. Allergy Clin. Immunol. 101:210-216(1998).  
 CC -!- FUNCTION: Destroys radicals which are normally produced within the  
 CC cells and which are toxic to biological systems (By similarity).  
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.  
 DR InterPro; IPR001424; SOD\_CU\_ZN.  
 DR Pfam; PF00080; sodcu; 1.  
 DR PROSITE; PS00087; SOD\_CU\_ZN\_1; PARTIAL.  
 DR PROSITE; PS00332; SOD\_CU\_ZN\_2; PARTIAL.  
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.  
 FT NON\_TER 29 29  
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17  
 |||  
 Db 7 LNS 9

# RESULT 27

## TL16\_SPIOL

ID TL16\_SPIOL STANDARD; PRT; 29 AA.  
 AC P81834;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leaf;  
 RX MEDLINE=98175931; PubMed=9506969;  
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;  
 RT "The thylakoid lumen of chloroplasts. Isolation and  
 RT characterization.";  
 RL J. Biol. Chem. 273:6710-6716(1998).  
 CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.  
 KW Chloroplast; Thylakoid.  
 FT NON\_TER 29 29

SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27  
|||  
Db 19 RKK 21

RESULT 28

DMS3\_PHYSA

ID DMS3\_PHYSA STANDARD; PRT; 30 AA.  
AC P80279;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Dermaseptin 3 (DS III).  
OS Phyllomedusa sauvagei (Sauvage's leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Phyllomedusa.  
OX NCBI\_TaxID=8395;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=94139686; PubMed=8306981;  
RA Mor A., Nicolas P.;  
RT "Isolation and structure of novel defensive peptides from frog skin.";  
RL Eur. J. Biochem. 219:145-154(1994).  
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST  
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE  
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
CC Dermaseptin subfamily.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.  
SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
|||  
Db 23 KKL 25

RESULT 29

FTN\_BACFR

ID FTN\_BACFR STANDARD; PRT; 30 AA.  
AC P28733;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ferritin like protein (Fragment).  
 OS Bacteroides fragilis.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=817;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=20656-2-1;  
 RX MEDLINE=92406001; PubMed=1526453;  
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;  
 RT "Isolation of a ferritin from Bacteroides fragilis."  
 RL FEMS Microbiol. Lett. 74:207-212(1992).  
 CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF  
 CC OXYGEN.  
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.  
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT  
 CC 17 kDa).  
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.  
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.  
 DR InterPro; IPR001519; Ferritin.  
 DR Pfam; PF00210; ferritin; 1.  
 DR PROSITE; PS50905; FERRITIN\_LIKE; 1.  
 KW Iron storage; Iron; Metal-binding.  
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.  
 FT METAL 17 17 IRON (BY SIMILARITY).  
 FT NON\_TER 30 30  
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQ 29  
 |||  
 Db 5 KLQ 7

#### RESULT 30

##### GLUM\_ANGAN

ID GLUM\_ANGAN STANDARD; PRT; 30 AA.  
 AC P41521;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Glucagon-like peptide (GLP).  
 OS Anguilla anguilla (European freshwater eel), and  
 OS Anguilla rostrata (American eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
 OC Anguilla.  
 OX NCBI\_TaxID=7936, 7938;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=A.anguilla, and A.rostrata;  
 RC TISSUE=Pancreas;  
 RX MEDLINE=91340068; PubMed=1874385;  
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;



RT "The primary structure of glucagon-like peptide but not insulin has  
RT been conserved between the American eel, *Anguilla rostrata* and the  
RT European eel, *Anguilla anguilla*.";  
RL Gen. Comp. Endocrinol. 82:23-32(1991).  
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
DR PIR; B61125; B61125.  
DR PIR; C61125; C61125.  
DR HSSP; P01275; 1BH0.  
DR InterPro; IPR000532; Glucagon.  
DR Pfam; PF00123; hormone2; 1.  
DR SMART; SM00070; GLUCA; 1.  
DR PROSITE; PS00260; GLUCAGON; 1.  
KW Glucagon family; Amidation.  
FT MOD\_RES 30 30 AMIDATION.  
SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQD 30  
|||  
Db 14 LQD 16

# RESULT 31

## OTCC\_AERPU

ID OTCC\_AERPU STANDARD; PRT; 30 AA.  
AC P11726;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)  
DE (Fragment).  
OS *Aeromonas punctata* (*Aeromonas caviae*).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; *Aeromonas*.  
OX NCBI\_TaxID=648;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NCIB 9232;  
RX MEDLINE=85104799; PubMed=3968036;  
RA Falmagne P., Portetelle D., Stalon V.;  
RT "Immunological and structural relatedness of catabolic ornithine  
RT carbamoyltransferases and the anabolic enzymes of enterobacteria.";  
RL J. Bacteriol. 161:714-719(1985).  
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate  
CC + L-citrulline.  
CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.  
DR InterPro; IPR006130; Asp/Orn\_Cotranf.  
DR InterPro; IPR006132; OTCace\_P.  
DR Pfam; PF02729; OTCace\_N; 1.  
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.  
KW Transferase; Arginine metabolism.  
FT NON\_TER 30 30

SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6  
|||  
Db 19 EIQ 21

RESULT 32

PCG2\_PACGO

ID PCG2\_PACGO STANDARD; PRT; 30 AA.  
AC P82415;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ponericin G2.  
OS Pachycondyla goeldii (Ponerine ant).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;  
OC Ponerinae; Pachycondyla.  
OX NCBI\_TaxID=118888;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Venom;  
RX MEDLINE=21264562; PubMed=11279030;  
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,  
RA Longeon A., Chafotte A., Dejean A., Rossier J.;  
RT "Ponericins, new antibacterial and insecticidal peptides from the  
RT venom of the ant Pachycondyla goeldii.";  
RL J. Biol. Chem. 276:17823-17829(2001).  
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE  
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL  
CC AND NON-HEMOLYTIC ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.  
KW Antibiotic; Insect immunity; Fungicide.  
SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24  
|||  
Db 11 EWL 13

RESULT 33

PCG3\_PACGO

ID PCG3\_PACGO STANDARD; PRT; 30 AA.  
AC P82416;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ponericin G3.  
 OS Pachycondyla goeldii (Ponerine ant).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;  
 OC Ponerinae; Pachycondyla.  
 OX NCBI\_TaxID=118888;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Venom;  
 RX MEDLINE=21264562; PubMed=11279030;  
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,  
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;  
 RT "Ponericins, new antibacterial and insecticidal peptides from the  
 RT venom of the ant Pachycondyla goeldii.";  
 RL J. Biol. Chem. 276:17823-17829(2001).  
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE  
 CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL  
 CC AND NON-HEMOLYTIC ACTIVITIES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.  
 KW Antibiotic; Insect immunity; Fungicide.  
 SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24  
 |||  
 Db 11 EWL 13

# RESULT 34

## PSAM\_PORPU

ID PSAM\_PORPU STANDARD; PRT; 30 AA.  
 AC P51395;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Photosystem I reaction centre subunit XII (PSI-M).  
 GN PSAM.  
 OS Porphyra purpurea.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
 OX NCBI\_TaxID=2787;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Avonport;  
 RA Reith M.E., Munholland J.;  
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast  
 RT genome.";  
 RL Plant Mol. Biol. Rep. 13:333-335(1995).  
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.

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DR EMBL; U38804; AAC08281.1; -.  
DR PIR; S73316; S73316.  
KW Photosystem I; Photosynthesis; Chloroplast.  
SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13  
|||  
Db 24 LGK 26

RESULT 35

TX2\_THRPR

ID TX2\_THRPR STANDARD; PRT; 30 AA.  
AC P83476;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Toxin ProTx-II.  
OS Thrixopelma pruriens (Green velvet).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Mygalomorphae; Theraphosidae; Thrixopelma.  
OX NCBI\_TaxID=213387;  
RN [1]  
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS  
RP SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Venom;  
RX MEDLINE=22363233; PubMed=12475222;  
RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,  
RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,  
RA Mehl J.T., Cohen C.J., Smith M.M.;  
RT "Two tarantula peptides inhibit activation of multiple sodium  
RT channels.";  
RL Biochemistry 41:14734-14747(2002).  
CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.  
CC Shifts the voltage-dependence of channel activation to more  
CC positive potentials.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.  
CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY  
CC TOXIN FAMILY.  
KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;  
KW Sodium channel inhibitor.  
FT DISULFID 2 16  
FT DISULFID 9 21  
FT DISULFID 15 25  
SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
|||  
Db 27 KKL 29

RESULT 36

UP61\_UPEIN

ID UP61\_UPEIN STANDARD; PRT; 30 AA.  
AC P82037;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Uperin 6.1.  
OS Uperoleia inundata (Floodplain toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=104953;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
RA Adams G.W., Severini C.;  
RT "Novel uperin peptides from the dorsal glands of the australian  
RT floodplain toadlet Uperoleia inundata.";  
RL Aust. J. Chem. 49:475-484(1996).  
CC -!- FUNCTION: UNKNOWN.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.  
KW Amphibian defense peptide.  
SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
|||  
Db 24 KKL 26

RESULT 37

UP62\_UPEIN

ID UP62\_UPEIN STANDARD; PRT; 30 AA.  
AC P82038;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Uperin 6.2.  
OS Uperoleia inundata (Floodplain toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104953;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
 RA Adams G.W., Severini C.;  
 RT "Novel uperin peptides from the dorsal glands of the australian  
 RT floodplain toadlet Uperoleia inundata.";  
 RL Aust. J. Chem. 49:475-484(1996).  
 CC -!- FUNCTION: UNKNOWN.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
 |||  
 Db 24 KKL 26

# RESULT 38

## VAA2\_EQUAR

ID VAA2\_EQUAR STANDARD; PRT; 30 AA.  
 AC Q04238;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)  
 DE (Fragment).  
 OS Equisetum arvense (Field horsetail) (Common horsetail).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.  
 OX NCBI\_TaxID=3258;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93138084; PubMed=8422915;  
 RA Starke T., Gogarten J.P.;  
 RT "A conserved intron in the V-ATPase A subunit genes of plants and  
 RT algae.";  
 RL FEBS Lett. 315:252-258(1993).  
 CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF  
 CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR  
 CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC  
 CC CELLS.  
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  
 CC H(+) (Out).  
 CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A  
 CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,  
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE  
 CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).

CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa  
 CC V-ATPASE SUBUNIT IN PSILLOTUM AND EQUISETUM.  
 CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.  
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 CC -----  
 DR EMBL; X56984; CAA40302.1; -.  
 DR PIR; S21815; S21815.  
 DR InterPro; IPR000194; ATPase\_a/bcentre.  
 DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; PARTIAL.  
 KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;  
 KW Multigene family.  
 FT NON\_TER 1 1  
 FT NON\_TER 30 30  
 SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MER 20  
 |||  
 Db 23 MER 25

# RESULT 39

Y523\_BORBU

ID Y523\_BORBU STANDARD; PRT; 30 AA.  
 AC O51473;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein BB0523.  
 GN BB0523.  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35210 / B31;  
 RX MEDLINE=98065943; PubMed=9403685;  
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,  
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,  
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,  
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,  
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,  
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,  
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,  
 RA Smith H.O., Venter J.C.;  
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia  
 RT burgdorferi.";

RL Nature 390:580-586(1997).  
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 CC -----  
 DR EMBL; AE001154; AAC66894.1; -.  
 DR PIR; B70165; B70165.  
 DR TIGR; BB0523; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21  
 |||  
 Db 26 ERV 28

# RESULT 40

CEC1\_PIG  
 ID CEC1\_PIG STANDARD; PRT; 31 AA.  
 AC P14661;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cecropin P1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90083227; PubMed=2512577;  
 RA Lee J.-Y., Boman A., Chuanxin S., Andersson M., Joernvall H., Mutt V.,  
 RA Boman H.G.;  
 RT "Antibacterial peptides from pig intestine: isolation of a mammalian  
 RT cecropin."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9159-9162(1989).  
 RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=93011123; PubMed=1396696;  
 RA Sipos D., Andersson M., Ehrenberg A.;  
 RT "The structure of the mammalian antibacterial peptide cecropin P1 in  
 RT solution, determined by proton-NMR."  
 RL Eur. J. Biochem. 209:163-169(1992).  
 CC !- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST  
 CC SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. ACTS BY A  
 CC NONPORE MECHANISM.  
 CC !- SUBCELLULAR LOCATION: Secreted.  
 CC !- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.



DR PIR; A36221; A36221.  
DR InterPro; IPR000875; Cecropin.  
DR Pfam; PF00272; cecropin; 1.  
DR PROSITE; PS00268; CECROPIN; 1.  
KW Antibiotic.  
SQ SEQUENCE 31 AA; 3339 MW; CB2B374A8B153850 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28  
|||  
Db 8 KKL 10

Search completed: January 14, 2004, 10:35:30  
Job time : 15.6137 secs